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Thanks,
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Result No.	Score	Query Match	Length	DB ID	Description
1	2275	100.0	422	4 Q16542	Q16542 homo sapien
2	1897	83.4	432	11 Q64385	Q64385 mus musculu
3	1871	82.2	432	11 P70225	P70225 mus musculu
4	1860.5	81.8	431	11 Q99mfa	Q99mfa ratus norv
5	391	17.2	372	11 Q88507	Q88507 mus musculu
6	269	11.8	228	11 Q35228	Q35228 mus musculu
7	259.5	11.4	229	4 Q75269	Q75269 homo sapien
8	255.5	11.2	229	4 Q14213	Q14213 homo sapien
9	215.5	9.5	881	13 Q57519	Q57519 xenopus lae
10	211.5	9.3	422	4 Q75462	Q75462 homo sapien
11	210.5	9.3	422	4 Q9UHH5	Q9UHH5 homo sapien
12	209.5	9.2	425	11 Q9jm58	Q9jm58 mus musculu
13	192	8.4	227	6 Q9GIW3	Q9GIW3 ursus marit
14	191	8.4	327	11 Q9et05	Q9et05 marmota mon
15	190.5	8.4	206	4 Q16354	Q16354 homo sapien
16	190.5	8.4	268	4 Q8Tcd78	Q8Tcd78 homo sapien

DR	EMBL; 246595; CAA86570.1; .;		
DR	EMBL; BC033110; AAH03110.1; .;		
DR	InterPro; IPR02996; CRIA.		
DR	InterPro; IPR03961; FN_III.		
DR	InterPro; IPR003530; Hemicooptn_L_F3.		
DR	InterPro; IPR03599; Ig.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	Pfam; PF00041; fn3; 2.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00060; FN3; 2.		
DR	SMART; SM00409; Ig; 1.		
DR	PROSITE; PS01354; HEMATopo_REC_L_F3; UNKNOWN_1.		
RW	Receptor.		
SQ	SEQUENCE 422 AA; 45222 MW; 1F8BC05C139FC326 CRC64;		
Query Match	100.0% Score 2275; DB 4; Length 422;		
Best Local Similarity	100.0% Pred. No. 9e-167;		
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 MSSCSGLSRVLYAVATALYSASSPCPQAWGPGVQYQOPGRSYKLCCPGVTAGDPVSWF 60		
DB	1 MSSCSGLSRVLYAVATALYSASSPCPQAWGPGVQYQOPGRSYKLCCPGVTAGDPVSWF 60		
Qy	61 RDGEPKLQGPDSGLGHLYLAQADSTDEGTYCQTLDALGGTVTQLGYPPARPVSC 120		
Db	61 RDGEPKLQGPDSGLGHLYLAQADSTDEGTYCQTLDALGGTVTQLGYPPARPVSC 120		
Qy	121 QAADDENFSCTWPSQISGLPTRLTSYRKTVLGADSDRSRSPSTGPWPCPQDPLGAARC 180		
Db	121 QAADDENFSCTWPSQISGLPTRLTSYRKTVLGADSDRSRSPSTGPWPCPQDPLGAARC 180		
Qy	181 VVHGAEEFWSOYRINTVEYNPLGASTRLDVSLSILRPDPQGLRVEVSPYQPRRLRASW 240		
Db	181 VVHGAEEFWSOYRINTVEYNPLGASTRLDVSLSILRPDPQGLRVEVSPYQPRRLRASW 240		
Qy	241 TYPASWPQPHFLKFLRQHPAWNTVEPAGLEEVTTDAVGLPHAVRYSARDFLD 300		
Db	241 TYPASWPQPHFLKFLRQHPAWNTVEPAGLEEVTTDAVGLPHAVRYSARDFLD 300		
Qy	301 AGTWSTWSPAWGTPSTGTKEPAWGLHTOPEVPODSDAPPRLSQQPLQPRLLDHR 360		
Db	301 AGTWSTWSPAWGTPSTGTKEPAWGLHTOPEVPODSDAPPRLSQQPLQPRLLDHR 360		
Qy	361 DSVEQAVIALSAGLTLSPFLGIVAGALGWLRLRGKDGSPKPGFLASVPIYDRRGAP 420		
Db	361 DSVEQAVIALSAGLTLSPFLGIVAGALGWLRLRGKDGSPKPGFLASVPIYDRRGAP 420		
Qy	421 NL 422		
Db	421 NL 422		
RESULT 2			
Q64385	PRELIMINARY; PRT; 432 AA.		
ID	Q64385; PRELIMINARY; PRT; 432 AA.		
AC	Q64385; PRELIMINARY; PRT; 432 AA.		
DT	01-JAN-1998 (TREMBlre. 05, Created)		
DT	01-MAR-2002 (TREMBlre. 05, Last sequence update)		
DE	Interleukin-11 receptor ALPHA chain 1 precursor (NR1) (ETL2)		
GN	IL11RA1 OR IL11RA OR ET12 OR ET12/IL11 REC.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TAXID=10090;		
RP	SEQUENCE FROM N_A.		
RC	STRAIN=C57BL/6 X CBA; TISSUE=LIVER;		
RC	MEDLINE=15045167; PubMed=9574545;		
RA	Hilton D.J., Hilton A.A., Raicevic A., Rakar S., Harrison-Smith M.		
RA	Gough N.M., Begley C.G., Metcalf D., Nicola N.A., Willson T.A.;		
RT	"Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130		
RT	for high affinity binding and signal transduction.";		
RL	EMBO J. 13:4765-4775(1994).		
RN	[2]		
RP	SEQUENCE FROM N_A.		
RC	STRAIN=BALB/c, AND C57BL/6; TISSUE=EMBRYO;		
RA	Neuhaus H., Beittenhausen B., Billinski P., Simon-Chazzottes D.,		
RA	Guenet J.L., Gossler A.		
RA	Dev. Biol. 166:521-542(1994).		
RN	[3]		
RP	SEQUENCE FROM N_A.		
RC	STRAIN=BALB/c, AND C57BL/6;		
RA	Gossler A.;		
RL	Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N_A.		
RX	MEDLINE=97129000; PubMed=8975540;		
RA	Billinski P., Hall M.A., Neuhaus H., Gissel C., Heath J.K., Gossler A.;		
RT	"Two differentially expressed interleukin-11 receptor genes in the mouse genome";		
RL	Biolog. J. 320:359-363(1996).		
RN	[5]		
RP	SEQUENCE FROM N_A.		
RA	Strauberg R.;		
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.		
CC	-!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11. BINDS TO IL-11.		
CC	-!- WITH LOW AFFINITY, BUT DOES NOT TRANSLATE A SIGNAL.		
CC	-!- SUBUNIT: HETEROODIMER OF AN ALPHA AND A BETA CHAIN.		
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	-!- TISSUE SPECIFICITY: WIDELY EXPRESSED.		
CC	-!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS ONE IG-LIKE DOMAIN.		
CC	-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.		
DR	EMBL; X74953; CAAS2908.1; -.		
DR	EMBL; U14412; AAA5248.1; -.		
DR	EMBL; X94162; CAA63873.1; -.		
DR	EMBL; X94163; CAA63873.3; JOINED.		
DR	EMBL; BC004619; AAH04619.1; -.		
DR	HSSP; P16471; 1BP3.		
DR	MGD; MGI:107416; 1BP3.		
DR	InterPro; IPR02996; CRIA.		
DR	InterPro; IPR0361; FN_III.		
DR	InterPro; IPR03530; Hantopoptn_L_F3.		
DR	InterPro; IPR03599; Ig.		
DR	InterPro; IPR03006; Ig_MHC.		
PFam	PF00044; fn3; 2.		
DR	InterPro; IPR0047; ig; 1.		
DR	SMART; SM00050; FN3; 2.		
DR	SMART; SM00409; IG; 1.		
DR	PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.		
KW	Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.		
FT	SIGNAL 1	23	POTENTIAL.
FT	INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1.		
FT	CHAIN 24	432	INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1.
FT	DOMAIN 24	367	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 368	393	POTENTIAL.
FT	DOMAIN 394	432	CYTOSMATIC (POTENTIAL).
FT	DOMAIN 41	102	IG-LIKE C2-TYPE DOMAIN.
FT	CARBOHYD 127	127	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 194	194	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE 432 AA;	46555 MW;	0683894350BBFC CRC64;
Query Match	83.4% Score 1897; DB 11; Length 432;		
Best Local Similarity	83.5%; Pred. No. 1e-137;		
Matches 355; Conservative 18; Mismatches 50; Indels 2; Gaps 1;			
QY	1 MSSSCGSLSRVLYAVATLYVASSPSCPQAWGPGVQYQOPGRSYKLCCPGVTAGDPVSWF 60		
Db	1 MSSSCGSLTRVLYAVATLYVASSPSCPQAWGPGVQYQOPGRSYKLCCPGVTAGDPVSWF 60		
QY	61 ROGEPKLQGPDSGLGHLYLAQADSTDEGTYCQTLDALGGTVTQLGYPPARPVSC 120		
Db	61 RDGDSRLQGPDSGLGHLYLAQADSTDEGTYCQTLDALGGTVTQLGYPPARPVSC 120		
QY	61 QAADDENFSCTWPSQISGLPTRLTSYRKTVLGADSDRSRSPSTGPWPCPQDPLGAARC 180		
Db	61 QAADDENFSCTWPSQISGLPTRLTSYRKTVLGADSDRSRSPSTGPWPCPQDPLGAARC 180		
QY	121 VVHGAEEFWSOYRINTVEYNPLGASTRLDVSLSILRPDPQGLRVEVSPYQPRRLRASW 240		
Db	121 VVHGAEEFWSOYRINTVEYNPLGASTRLDVSLSILRPDPQGLRVEVSPYQPRRLRASW 240		
QY	241 TYPASWPQPHFLKFLRQHPAWNTVEPAGLEEVTTDAVGLPHAVRYSARDFLD 300		
Db	241 TYPASWPQPHFLKFLRQHPAWNTVEPAGLEEVTTDAVGLPHAVRYSARDFLD 300		
QY	301 AGTWSTWSPAWGTPSTGTKEPAWGLHTOPEVPODSDAPPRLSQQPLQPRLLDHR 360		
Db	301 AGTWSTWSPAWGTPSTGTKEPAWGLHTOPEVPODSDAPPRLSQQPLQPRLLDHR 360		
QY	361 DSVEQAVIALSAGLTLSPFLGIVAGALGWLRLRGKDGSPKPGFLASVPIYDRRGAP 420		
Db	361 DSVEQAVIALSAGLTLSPFLGIVAGALGWLRLRGKDGSPKPGFLASVPIYDRRGAP 420		
QY	421 NL 422		
Db	421 NL 422		

Db 121 QAVDYEENFSCTWSPGQVSGLEPTRYLTSRKKTLPGAESQRESSTGPWPCCPDPLEASRC 180
 Qy 181 VVHGAEEWSQRINTEVNPPIGASTRDLDSLQSLRDPDPQGLVESVGYPRLRASH 240
 Db 181 VVHGAEEWSERINTEVNPPIGASTRDLDSLQSLRDPDPQGLVESVGYPRLRASH 240
 Qy 241 TYPASWPCQPHFLKERLQRPAQHPAWSITVEPAGLEEVITDAVGLPHAVRSARDFLD 300
 Db 241 TYPASWPCQPHFLKERLQRPAQHPAWSITVEPAGLEEVITDAVGLPHAVRSARDFLD 300
 Qy 301 AGTWSWSPEAWGTPPTGTLPKEIPAWGQHTQ--PEVEQVQDSAPPAPPSLQPHPRLLD 358
 Db 301 AGTWSWSPEAWGTPPTGTLPKEIPAWGQHTQ--PEVEQVQDSAPPAPPSLQPHPRLLD 360
 Qy 359 HRDSVQAVAVASLGILSFLGLVAGALALGWLRLRRGGDGSPPPGFTASVYIPDRPG 418
 Db 361 HRDPLQEVAVLASLGIFSCLGIFSCLGIFSCLGIFSCLGIFSCLGIFSCLGIFSCLG 420
 Qy 419 APNL 4.22
 Db 421 IPNL 4.24

RESULT 3

P70225 ID P70225 PRELIMINARY; PRT; 432 AA.
 AC P70225; 000074;
 DT 01-FEB-1997 (TRIMBLrel. 02, Created)
 DT 01-FEB-1997 (TRIMBLrel. 02, Last sequence update)
 DT 01-MAR-2002 (TRIMBLrel. 20, Last annotation update)
 DE Interleukin-11 receptor alpha chain 2 precursor (IL11RA2) (IL-11RBETA)
 DE (Interleukin-11 receptor beta chain).
 GN IL11RA2 OR IL-11RBETA.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N.A.
 RN STRAIN=CDL; TISSUE=TESTIS;
 RX MEDLINE=97129000; PubMed=8973540;
 RA Billings P., Hall M.A., Neuhaus H., Gissel C., Heath J.K., Gossler A.;
 RT "Two differentially expressed interleukin-11 receptor genes in the mouse genome.";
 RT Biochem. J. 320:359-363 (1996).
 RN [2] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=TESTIS;
 RX MEDLINE=962778810; PubMed=8662602;
 RA Robb L., Hilton D.J., Willison T.A., Begley C.G.;
 RT "Structural analysis of the gene encoding the murine interleukin-11 receptor alpha-chain and a related locus.";
 RL J. Biol. Chem. 271:13754-13761 (1996).
 RN [3] SEQUENCE FROM N.A.
 RP SEQUENCE=CD-1; TISSUE=TESTIS;
 RX MEDLINE=97230451; PubMed=9073505;
 RA Robb L., Hilton D.J., Brook-Carter P.T., Begley C.G.;
 RT "Identification of a second murine interleukin-11 receptor gene (IL11Ra2) with a restricted pattern of expression.";
 RL Genomics 40:387-394 (1997).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.
 CC -1- SUBUNIT: HETEROODIMER OF AN ALPHA AND A BETA CHAIN.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.

DR HSSP; P164471; 1BP3.
 DR MGI; MGI:109123; 1111ra2.
 DR InterPro; IPR002996; CR1A.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR003530; Hemtopoptin_L_F3.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00041; fn3; 2.
 DR Pfam; PE00047; iq; 1.
 DR SMART; SMO0060; FN3; 2.
 DR SMART; SMO0409; IG; 1.
 DR PROSITE; PS01354; HENATOPO_REC_L_F3; UNKNOWN 1.
 KW Glycoprotein; Immunoglobulin domain; Receptor; Signal; Transmembrane.
 FT CHAIN 24 432 INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 2.
 FT DOMAIN 24 367 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 368 393 POTENTIAL.
 FT DOMAIN 394 432 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 41 102 IC-LIKE C2-TYPE DOMAIN.
 FT CARBOHYD 127 N-LINKED (GLCNAC, .) (POTENTIAL).
 FT CARBOHYD 194 194 N-LINKED (GLCNAC, .) (POTENTIAL).
 FT CONFLICT 200 200 S -> P (IN CAA63872).
 FT CONFLICT 384 384 V -> L (IN CAA63872).
 SQ SEQUENCE 432 AA; 46721 MW; 0D8E49723EC99EC5 CRC64;

Query Match Score 82.2%; Score 1871; DB 11; Length 432;
 Best Local Similarity 82.5%; Pred. No. 9.9e-136;
 Matches 350; Conservative 19; Mismatches 53; Indels 2; Gaps 1;

Qy 1 MSSSCSGLSRVLYAVATLYSASSPQCAWGPQPGYQGPERSVYKLCCPGVYTAGDPVSWF 60
 Db 1 MSSSCSGLTRVLYAVATLYSASSSPCPQAWGPQPGYQGPERSVYKLCCPGVYTAGDPVSWF 60
 Qy 61 RDGEPEKLLQGDPSGLGHELVLAQAQSTDDEGYICQNDGAGTTVNLQGYPPARPVSC 120
 Db 61 RDGDSRLLQGDPSGLHRVLAQVDPSDEGTIVCQTDGSGMVYLKLGPAREPVSC 120
 Qy 121 QAADDYENFSCTWSPSQISGLPTRYLTSYRKTVLGADSQRSPSTGPWPCQDPLGAARC 180
 Db 121 QAVDYNENFSCTWSPSQISGLPTRYLTSYRKTVLGADSQRSPSTGPWPCQDPLGAARC 180
 Qy 181 VHGAEEFWSEYRINVTENVNPLGASTRLDVSLSQSLTRDPFQGLRVESYVPYRRLRASW 240
 Db 181 VHGAEEFWSEYRINVTENVNLSGASTCLLDVRLQSIIRDPFQGLRVESYVPYRRLRASW 240
 Qy 241 TYPASWPCOPHFLKRLQYPAQHAWSTVEPAGIEEVITDAVGLPHAVRVSARDFLD 300
 Db 241 TYPASWPCOPHFLKRLQYPAQHAWSTVEPAGIEEVITDAVGLPHAVRVSARDFLD 300
 Qy 301 AGTWSWSPEAWGTPPTGTLPKEIPAWGQLEITQ--PEVEPOVDSAPPAPRSLQPHRLD 358
 Db 301 AGTWSWSPEAWGTPPTGTLPKEIPAWGQLEITQ--PEVEPOVDSAPPAPRSLQPHRLD 358
 Qy 359 HRDSVEQAVLASGILSFLGLVAGALGWLRLRGKGDKSPKGFLASVIPYDPRPG 418
 Db 361 HRDPLQEAVLASGILSFLGLVAGALGWLRLRGKGDKSPKGFLASVIPYDPRPG 420

RESULT 4

Q9MF4 ID Q9MF4 PRELIMINARY; PRT; 431 AA.
 AC Q9MF4; 099MF4
 DT 01-JUN-2001 (TRIMBLrel. 17, Created)
 DT 01-JUN-2001 (TRIMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TRIMBLrel. 20, Last annotation update)
 DE Interleukin 11 receptor alpha chain.
 OS Rattus norvegicus (rat).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC

OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	[1] NCBITAXID=10116;
RC	SEQUENCE FROM N.A.
RA	"Sprague-Dawley,"
RA	Li R., Hartley L., Robb L.;
RT	"Expression of interleukin-11 and interleukin-11 receptor alpha chain in the rat uterus in the peri-implantation period.";
RT	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AF247936; AAK29624; 1.;
DR	HSSP; P16471; 1BP3.
DR	InterPro; IPR002996; CRIA.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR003510; Hemtopoptn_L_F3.
DR	InterPro; IPR003590; Ig.
DR	InterPro; IPR003600; Ig-like.
DR	InterPro; IPR003606; Ig_MHC.
DR	Pfam; PF00041; fn3; 2.
DR	PFAM; PF00047; fn3; 1.
DR	SMART; SM00050; FN3; 2.
DR	SMART; SM00409; Ig; 1.
DR	SMART; SM00410; Ig-like; 1.
DR	PROSITE; PS01354; HEMATopo_REC_L_F3; UNKNOWN_1.
KW	Receptor.
SQ	431 AA; 46784 MW; E086FD6B1688180B CRC64;
Query Match	81.8%; Score 1860.5; DB 11; Length 431;
Best Local Similarity	82.0%; Pred. No. 6.3e-135;
Matches	347; Conservative 21; Mismatches 54; Indels 1; Gaps 1;
Qy	1 MSSSCSGLSRVLYAVATALVASSSPCCPAQAWGPVGVOYQGPGRSVKLCCPGVYTAGDPVSWF 60
Db	1 MSSSRSGLTRVLYAVATALVASSSTPCPAQAWGPVGVOYQGPGRSVKLCCPGVYTAGDPVSWF 60
Qy	61 RDGEPKLLQPGDGLGLHFLVLQAQDSDEGTYCOTDGALGTVTLQLGYFPARPVSC 120
Db	61 RDGDSRLLQPGDGLGLHFLVLQAQDSDEGTYCOTDGALGTVTLQLGYFPARPVSC 120
Qy	121 QADDYENFSCTWSPSQISGLPRLYLTSYRKTKTLYLGASQRRSPSTGPWPCCPDPLGARC 180
Db	121 QADYENFSCTWSPSQISGLPRLYLTSYRKTKTLYLGASQRRSPSTGPWPCCPDPLGARC 180
Qy	181 VHGAEFMSQYRINTEVNPLGASTRLDVQSOSIRLPDPGQLRVEVPGVYPRRLRASW 240
Db	181 VHGAEFMSQYRINTEVNPLGASTRLDVQSOSIRLPDPGQLRVEVPGVYPRRLRASW 240
Qy	241 QTYASWRQPHFLKFLKFLQYRAQHPAWSTVPAQLEVITDAVGLPHAVYRSARDFLD 300
Db	241 QTYASWRQPHFLKFLKFLQYRAQHPAWSTVPAQLEVITDAVGLPHAVYRSARDFLD 300
Qy	301 AGTWSTNSPEANGTPSTGTTKEIPANGQLHTQP-EVEPOVQSPAPPRPSLQPHPRLDH 359
Db	301 AGTWSTNSPEANGTPSTGTTKEIPANGQLHTQP-EVEPOVQSPAPPRPSLQPHPRLDH 360
Qy	360 ROSVEQAVLAVSLGJLSPGLVAGAIALGLWLRRLRGKGDKGPKGFLASVTPVDRRPGA 419
Db	361 RDPLEQAVLAVSLGJLSPGLVAGAIALGLWLRRLRGKGDKGPKGFLASVTPVDRRPGA 420
Qy	420 PNL 422
Do	421 PNL 423
RESULT 5	PRELIMINARY; PRT; 372 AA.
OBB507	PRELIMINARY; PRT; 372 AA.
AC	OB8507;
DT	01-NOV-1998 (TREMBLrel. 08. Created)
DT	01-MAR-2002 (TREMBLrel. 20. Last annotation update)
DT	Ciliary neurotrophic factor receptor alpha precursor.
GN	[1]_TAXID=10090;
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mus musculus (Mouse).
RA	Nomura H., Yaguchi N., Hanyuu C., Maeda M., Kikuchi Y., Nakata Y.,
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	SEQUENCE FROM N.A.
RC	TISSUE=RAIN.
RA	Meda M., Yaguchi N., Hanyuu C., Nakata Y., Nomura H.,
RA	Kojima T., Hasegawa M., Kikuchi Y., Nomura H.;
RT	"Mouse homolog of human ciliary neurotrophic factor receptor."
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF068615; AAC25711.1; -.
DR	MG1; MG1:99605; Cntfr.
DR	InterPro; IPR002996; CRIA.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR003590; Ig.
DR	InterPro; IPR003590; Hemtopoptn_L_F3.
DR	InterPro; IPR003598; Ig_c2.
DR	InterPro; IPR003006; Ig_MHC.
DR	Pfam; PF00041; fn3; 2.
DR	PFAM; PF00047; fn3; 1.
DR	SMART; SM00050; FN3; 1.
DR	SMART; SM00409; Ig; 1.
DR	SMART; SM00410; Ig-like; 1.
DR	PROSITE; PS01354; HEMATopo_REC_L_F3; UNKNOWN_1.
KW	Immunoglobulin domain; Receptor; Signal.
FT	POTENTIAL.
FT	CHAIN
FT	ALPHA.
SQ	SEQUENCE 372 AA; 40831 MW; EB75A9BE6A1B8C8 CRC64;
Query	Match 17.2%; Score 391; DB 11; Length 372;
Best Local Similarity	31.8%; Pred. No. 3.9e-22;
Matches	113; Conservative 49; Mismatches 163; Indels 30; Gaps 12;
Qy	1 MSSSCSGLSRVLYAVATALVASSSPCCPAQAWGPVGVOYQGPGRSVKLCCPGVYTAGDPVSWF 60
Db	1 MTASVPRACAVLAARAAAVITQKHSQPE - APHQVQEIRLGADVTIPLCGTASWDAVWTW 58
Qy	61 RDGEPKLLQPGDGLGLHFLVLQAQDSDEGTYCOTDGALGTVTLQLGYFPARPVVS 120
Db	61 RDGDSRLLQPGDGLGLHFLVLQAQDSDEGTYCOTDGALGTVTLQLGYFPARPVVS 120
Qy	121 QADDYENFSCTWSPSQISGLPRLYLTSYRKTKTLYLGASQRRSPSTGPWPCCPDPLGARC 180
Db	121 QADYENFSCTWSPSQISGLPRLYLTSYRKTKTLYLGASQRRSPSTGPWPCCPDPLGARC 180
Qy	181 VHGAEFMSQYRINTEVNPLGASTRLDVQSOSIRLPDPGQLRVEVPGVYPRRLRASW 240
Db	181 VHGAEFMSQYRINTEVNPLGASTRLDVQSOSIRLPDPGQLRVEVPGVYPRRLRASW 240
Qy	241 QTYASWRQPHFLKFLKFLQYRAQHPAWSTVPAQLEVITDAVGLPHAVYRSARDFLD 300
Db	241 QTYASWRQPHFLKFLKFLQYRAQHPAWSTVPAQLEVITDAVGLPHAVYRSARDFLD 300
Qy	301 AGTWSTNSPEANGTPSTGTTKEIPANGQLHTQP-EVEPOVQSPAPPRPSLQPHPRLDH 359
Db	301 AGTWSTNSPEANGTPSTGTTKEIPANGQLHTQP-EVEPOVQSPAPPRPSLQPHPRLDH 360
Qy	360 ROSVEQAVLAVSLGJLSPGLVAGAIALGLWLRRLRGKGDKGPKGFLASVTPVDRRPGA 419
Db	361 RDPLEQAVLAVSLGJLSPGLVAGAIALGLWLRRLRGKGDKGPKGFLASVTPVDRRPGA 420
Qy	420 PNL 422
Do	421 PNL 423
RESULT 6	PRELIMINARY; PRT; 228 AA.
ID	035228
AC	OB8507 OR EBI3.
DT	01-JAN-1998 (TREMBLrel. 05, Created)
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE	Cytokine receptor-like molecule (Epstein-Barr virus induced gene DE)
GN	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TAXID=10090;
RP	SEQUENCE FROM N.A.
RA	Nomura H., Yaguchi N., Hanyuu C., Maeda M., Kikuchi Y., Nakata Y.,

RESULT 9
 ID 057519 PRELIMINARY; PRT; 881 AA.
 AC 057519; PRT; 881 AA.
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE GP13Op_1.
 GN XGP13Op_1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Amphibia; Batrachia; Craniata; Vertebrata; Buteleostomi;
 OC Xenopodidae; Xenopus.
 NCBI_TAXID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Macrangeas F.; Jacques Y.; Minvielle S.;
 RT "Cloning and expression of a novel soluble protein containing
 hematopoietic cytokine receptor domains.";
 RT Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF059233; ANC28335.1;
 DR EMBL; AF073515; ADD39681.1; -.
 DR HSSP; P16471; 1BP3.
 DR InterPro; IPR002996; CRIA.
 DR InterPro; IPR03961; FN_III.
 DR Pfam; PF00041; fn3; 2.
 DR SMART; SM00060; FN3; CRC64;
 DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
 SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D211138A0 CRC64;
 Query Match 9.5%; Score 215.5; DB 13; Length 881;
 Best Local Similarity 23.3%; Pred. No. 3.3e-08;
 Matches 88; Conservative 61; Mismatches 145; Indels 83; Gaps 19;

Query Match 9.3%; Score 211.5; DB 4; Length 422;
 Best Local Similarity 23.7%; Pred. No. 2.7e-08;
 Matches 91; Conservative 53; Mismatches 145; Indels 95; Gaps 19;

Query 7 GLSRVLVAVATLYSASSSPCPQANGPPGQYQGPGRSYKLCC----PGVTAGDPV/SWF 60
 Db 30 GAFRAGSGAHTAVLSPQOPTLLI-----GSSLATCSYHGDOPGATA-EGLYWT 77
 Qy 61 RDGE--PKLQLQSPDSGLGHELVLAQAD----STDECTYICOTLDGAQGTIVTLQLYP 112
 Db 78 LNRRLPPELSRVLNAS---TIALALANLNGSRQRSGDNLVCHARDGSILAGSCLYVGLP 134
 Qy 113 PARPV-VSQQAADYENFSCWTSQPSQ-----TSLGLPRYLSSYRKTVLGARSQRSRSPSTGWP 169
 Db 135 PERPVNICSWSKMNKDLICRWTFGAHGTFLHTNLYKLRMYQDNTCEEEYHTVGH 194
 Qy 170 C-PQDPGLGAARCYVHGAELFSQYRINTVEVNPLG-ASTRLDVLSQSLRDPPOGJRV 226
 Db 195 CHIPKD-----LALFTYEINWEATNRLGSASTDVLTDIUVYTDPPIPWHV 243
 Qy 227 ESYPGYPRPLRASWTPSPWPCOPPHILL--KFRLQYRAQHPAWSTVP-----AG 275
 Db 244 SRVGGLEQOLPSRVWSP--PALKDFLEQAKYQIRYRVEDSYDWKVVVDVSNOTSCRLAG 300
 Qy 276 LEVITDAGLPHAVYRSARDE----LDAGTWSTNS-PEA----- 311
 Db 301 L-----PGTVYFVQRCNPFGIYGGSKKAGIWSHENHPTAASTPRSERPGRGGGACEP 353
 Qy 312 -WGTGSTGTKEIP--AWGQHL 331
 Db 354 RGGEPSSCPVRRELKQFGWLKH 377
 Qy 327 WQGLHTQPPVEPOVDSP 343
 Db 323 -----PDIWKKIDSP 332

RESULT 11

Q9UHH5	PRELIMINARY;	PRT;	422 AA.	
ID Q9UHH5;				
AC Q9UHH5;				
DT 01-MAY-2000 (TREMBLrel. 13, Created)				
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE Class I cytokine receptor.				
GN ZCYTOS5.				
OS Homo sapiens (Human).				
RA Foster D.C.; Presnell S.R.; Jelmingberg A.C.; Gilbert T.; Whitmore T.E., Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.				
OC NCBI_TAXID=9606;				
OX [1]				
RN				
SEQUENCE FROM N.A.				
RA Lok S., Presnell S.R., Jelmingberg A.C., Gilbert T., Whitmore T.E., Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.; Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.				
RL DR EMBL; AF178684; AAD5385; 1.; -.				
DR SMART; SM00060; FN3; 2.				
KW Receptor.				
DR InterPro; IPR02996; CR1A.				
DR InterPro; IPR02996; FN_III.				
DR PFAM; PF00041; fn3; 2.				
DR SMART; SM00060; FN3; 1.				
RN				
SEQUENCE FROM N.A.				
RA Lok S., Presnell S.R., Jelmingberg A.C., Gilbert T., Whitmore T.E., Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.; Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.				
RL DR EMBL; AF178684; AAD5385; 1.; -.				
DR SMART; SM00060; FN3; 2.				
KW Receptor.				
DR InterPro; IPR02996; CR1A.				
DR InterPro; IPR02996; FN_III.				
DR PFAM; PF00041; fn3; 2.				
DR SMART; SM00060; FN3; 2.				
RN				
SEQUENCE	422 AA;	46315 MW;	0D2C5F7A01B942EE CRC64;	
Query Match	9.3%;	Score 210.5;	DB 4;	Length 422;
Best Local Similarity	23.7%;	Pred. No. 3.3e-08;		
Matches	91;	Conservative	53;	Mismatches 145; Indels 95; Gaps 19;
Qy	7 GLSRVLYAVATAVASSPCPQAQGPPGVYQGPGRSVKLCC-----PVVTAGDPVSWF 60			
Db	30 GAPRASSGAHTAVISQDPFLLI-----GSLLATCSCVHGDPPGATA-GSLYNW 77			
Qy	61 RDGE---PKLQQPDGSLGHELVLQAOD-----SDEGTYTICQTLDALGGTVTLQLGYP 112			
Db	78 LNRRLLPPELSRVLNAS---TLALALANLNGSQRSGDNLYCHARDGCSILAGSCLVYGLP 134			
Qy	113 PARPV-VSCQADYEFNSCWTPSPQ - ISGLPTRYLTSYRKTVLGADSQRSPSTGPWP 169			
Db	135 PEKPVNTWSKSNMKDLTCRTPGAHGETLHTNYSLKVKLRYQDNTCEEYHVGPHS 194			
Qy	170 C-PQDPLGAAARCVVHGAEFWSQYRINVTENVPNLG-ASTRLDVLSQSLRDPDPOGLRV 226			
Db	195 CHIPKD-----LALETPYEIWWEATNRLGSGARSVDLTDILDVTTDPPEDEVH 243			
Qy	227 ESVPGYPRRLRASWTPASNPQCOPHFLI--KFRLQYRPAQHPAWSTVEP-----AG 275			
Db	244 SRVGGLEDQLSVRWVSP---PALKDFLFLQAKYQIRYVEDSDVWKVYDDVSNOTSCRLAG 300			
Qy	276 LEEVITDAVAGLPHAVRSADF----LDAGTWSTWS-PBA-----AG 311			
Db	301 LK-----PCTVYFVQRCNPFGIYGSKAKIWTSEWSHPTAASTPRSERPGGGACEP 353			
Qy	312 -WGTGSTGTIPREIP--ANGQOL 331			
Db	354 RGEPSSGPVRELKQFLGLNKKH 377			
RESULT	12			
Q9JM58	PRELIMINARY;	PRT;	425 AA.	
ID Q9JM58;				
AC Q9JM58;				
DT 01-OCT-2000 (TREMBLrel. 15, Created)				
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)				
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)				
DE Cytokine receptor like molecule 3 precursor.				
GN CRLF1 OR CRM3.				
OS Mus musculus (Mouse).				
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.				
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Murinae.				
OX NCBI_TAXID=10090;				
RN [1]				
RP SEQUENCE FROM N.A.				
RA Hiroyama T., Iwama A., Nakamura Y., Nakuchi H.; "cytokine receptor like molecule 3."				
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
RL DR AB00038; BA9277; 1.; -.				
DR HSSP; P16471; IBP3.				
DR MGI; MGI:1440030; Crf1.				
DR InterPro; IPR02996; CR1A.				
DR InterPro; IPR02996; FN_III.				
DR PFAM; PF00041; fn3; 2.				
DR SMART; SM00060; FN3; 1.				
KW Receptor; Signal.				
FT SIGNAL	1	34	POTENTIAL.	
SQ SEQUENCE	425 AA;	46662 MW;	910535C629CA7056 CRC64;	
Query Match	9.2%;	Score 209.5;	DB 11;	Length 425;
Best Local Similarity	23.9%;	Pred. No. 3.9e-08;		
Matches	89;	Conservative	53;	Mismatches 138; Indels 93; Gaps 18;
Qy	17 TALVASSSPCPOAAGPGVQYQGPGRSVKLCC-----PGVTAGDGVFSWFRDGEPKLQG 70			
Db	43 TAVISQDQPTLII-----GSSLQATCSTHSIDTPGATA-EGLYWTNG - FRLPS 88			
Qy	71 PDSGLGHEHLVLAQADSTDEGT-----YICOTLDALGGTVTOLQYPPARPV-VSCQA 122			
Db	89 ELSRLNNTSTLALANLNGSROQSDNLYCHARDGSILAGSCLVYGLPPEKPFN1SCWS 148			
Qy	123 ADYENFSCTRWPSQ - ISGLPTRYLTSYRKTVLGDSORSPSPCPWPC - PODPIGAA 178			
Db	149 RNMKDTCRWTGAAHGTFLTNYSKYKLVWQNTCEYHTVPHSPHSCHIPKD----- 203			
Qy	179 RCVVHCAFEWQSOYRINVTENVPNLG - ASTRLDVLSQSLIRLDPDQQLRVEVPGVYPRRLR 237			
Db	204 -----LALETPYEIWWEATNRLGSGARSVDLTDILDVVTIDPPIPVHVSRVGGLEDQLS 257			
Qy	238 ASWTYPASWPCOPHFLI - KFRLQYRPAQHPAWSTVEP-----AGLEVITAVAG 286			
Db	258 VRWVSP -- PALKDFLFLQAKYQIRYVEDSDVWKVYDDVSNOTSCRLAGLK -----PG 307			
Qy	287 LPHAVVSVARDF-----LDACTWSWS-PEA-----WGTGSTGTIP 321			
Db	308 TVYFVYRCNPFGIYSSKAKIWESENHSPTAASTRPSSERPGPGGYCEPRGGEPSGPVR 367			
Qy	322 KEIP-----AWGQLH 331			
Db	368 RELKQFLGWLRKH 380			
RESULT	13			
Q9GLW3	PRELIMINARY;	PRT;	227 AA.	
ID Q9GLW3				
AC Q9GLW3;				
DT 01-MAR-2001 (TREMBLrel. 16, Created)				
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE Prolactin receptor (Fragment)				
OS Ursus maritimus (Polar bear)				
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Buteraria; Carnivora; Fissipedia; Ursidae; Ursus.				
OX NCBI_TAXID=29073;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC TISSUE-LIVER;				
RX MEDLINE=20086658; PubMed=10618852;				
RA Howell-Skalla L.A., Funick D., Bleck G.T., Nelson R.A., Bahr J.M.;				
RT Cloning and sequence analysis of the extracellular region of the polar bear (Ursus maritimus) luteinizing hormone receptor (LHR), follicle stimulating hormone receptor (FSHR), and prolactin receptor (PRLR) genes and their expression in the testis of the black bear (Ursus americanus).				
RT Mol. Reprod. Dev. 55: 136-145 (2000).				
RL EMBL; AF169792; AAC10648.1; -.				
DR HSSP; P14787; LAN3.				

Sat Jan 18 21:53:46 2003

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Search completed: January 17, 2003, 19:39:09
Job time : 45 secs

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Scoring table:	BLOSUM62		
Gapopen	10.0		
Gapext	0.5		
Searched:	112892 seqs, 41476328 residues		
Total number of hits satisfying chosen parameters:	112892		
Minimum DB seq length:	0		
Maximum DB seq length:	2000000000		
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries		
Database :	SwissProt_40_*		
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES			
Result No.	Score	Query Match	Description
Length	DB ID	%	
1	395.5	17.4	P22272 mus musculus
2	392	17.2	Q08406 ratus norvegicus
3	390.5	17.2	P22273 ratus norvegicus
4	382	16.8	P26692 homo sapiens
5	381	16.7	P31641 gallus gallus
6	360	15.8	P08887 homo sapiens
7	326.5	14.4	Q18796 sus scrofa
8	234	10.3	Q91094 melaleuca gummifera
9	221	9.7	O90374 columba livia
10	214	9.4	Q04594 gallus gallus
11	203.5	9.2	O46561 ovis aries
12	204.5	9.0	P28172 bos taurus
13	204	9.0	P14787 orctoceratops
14	197.5	8.7	Q28235 cervus elaphus
15	190	8.4	Q61729 marmota monax
16	190	8.4	Q02815 ovis aries
17	189	8.3	P16471 homo sapiens
18	186	8.2	Q03696 gallus gallus
19	184	8.1	P46282 bos taurus
20	183	8.0	Q28234 cervus elaphus
21	183	8.0	P05710 ratus norvegicus
22	174.5	7.7	Q28938 sus scrofa
23	174.5	7.7	P002744 felis silvestris
24	174	7.6	Q08501 mus musculus
25	173.5	7.6	Q91513 oreochromis
26	167.5	7.4	P29460 homo sapiens
27	166.5	7.3	P13592 homo sapiens
28	164.5	7.2	P48095 macaca mulatta
29	164	7.2	Q9xsg5 equus caballus
30	150	6.6	P40189 homo sapiens
31	149.5	6.6	Q9qz77 mus musculus
32	148.5	6.5	P42703 homo sapiens
33	148	6.5	P16882 mus musculus

ALIGNMENTS

RESULT 1					
IL6A_MOUSE	STANDARD;	PRT;	460 AA.		
ID P22272;					
AC P22272;					
DT 01-AUG-1991 (Rel. 19, Created)					
DT 01-AUG-1992 (Rel. 23, Last sequence update)					
DT 16-OCT-2001 (Rel. 40, Last annotation update)					
DE Interleukin-6 receptor alpha chain precursor (IL-6R 1).					
GN IL6RA OR IL6R.					
OS Mus musculus (Mouse)					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.					
OX NCBI_TaxID=10090;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=BALB/C; TISSUE=Spleen;					
RX MEDLINE-90278354; PubMed-2112585;					
RA Sugita T., totsuka T., Saito M., Yamasaki K., Taga T., Hirano T.,					
RA Kishimoto T.;					
RT "Functional murine interleukin 6 receptor with the intracellular A particle gene product at its cytoplasmic domain. Its possible role in plasmacytogenesis."					
RT J. Exp. Med. 171:2001-2009(1990).					
RL P22272					
RN [2]					
RP SEQUENCE FROM N.A.					
RC STRAIN=C3H; TISSUE=Liver;					
RA Florillo M.T., Ciliberto G., Dentte L.;					
RA Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.					
RL -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6 BINDS TO IL-6 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE REACTIONS AND HEMATOPOEISIS.					
CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY SIMILARITY).					
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.					
CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.					
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.					
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.					
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.					
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
DR X51623					
DR X53802					
DR XAA37830.1;					
DR PIR; JL0144;					
DR PIR; JL0145;					
DR PIR; S14543;					
DR HSSP; P16471; IBP3.					

DE	Ciliary neurotrophic factor receptor alpha precursor (CNTFR alpha).
GN	CNTFR.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathia; Murinae; Rattus.
OX	NCBI_TAXID:10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RC	SEQUENCE OF 185-277 FROM N.A.
RC	STRAIN=Sprague-Dawley; TISSUE=Brain;
RC	MEDLINE=93152175; PubMed=8381290;
RC	IP_N.Y.; McClain J.; Barrezueta N.X.; Aldrich T.H.; Pan L.; Li Y.;
RA	Wiegand S.J.; Friedman B.; Davis S.; Yancopoulos G.D.;
RA	"The alpha component of the CNTF receptor is required for signaling
RT	development." RT and defines potential CNTF targets in the adult and during
RT	development [1].
RN	Neuron 10:89-102(1993).
RN	[2]
RP	SEQUENCE OF 185-277 FROM N.A.
RC	Clatterbuck R.E., Price D.L., Koliatos V.E.
RC	"Ciliary neurotrophic factor prevents retrograde neuronal death in the adult central nervous system";
RC	Proc. Natl. Acad. Sci. U.S.A. 90:2222-2226(1993).
RC	-!- FUNCTION: BINDS TO CNTF (GPA). THE ALPHA CHAIN PROVIDES THE RECEPTOR SPECIFICITY.
CC	-!- SUBUNIT: HETEROTRIMER OF THE ALPHA CHAIN, LIFR AND GP130.
CC	-!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC	-!- TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC	-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC	-!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC	-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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DR	S5212; AAB2290_1; -.
DR	S5771; AAB22918_1; -.
DR	A47387; A7387.
DR	IPRO02996; CRIA.
DR	IPRO03961; FN_III.
DR	IPRO03530; Hemtopoptn_L-F3.
DR	IPRO03006; Ig_MHC.
DR	IPRO03598; Ig_C2.
DR	PFam: PF00041; fn3; 1.
DR	SMART: SM00060; FN3; 1.
DR	SMART: SM00408; IgC2; 1.
DR	PROTEP: PS01354; HEMATopo_REC_L_F3; 1.
KW	Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.
FT	SIGNAL
FT	CHAIN
FT	PROPEP
FT	DOMAIN
FT	DISULFID
FT	CARBHYD
FT	LIPID
SQ	SEQUENCE
391	-----GSPKGFLASVTPVDRRGAPN 421
392	-----VAGGSTLPGLLLCV 381
393	-----ANHEQYESSSTEAVYLQVQESSMSLRL-VAGGSTLPGLLLCV 381
394	-----GLPKPTFLVPLLTHPSSGSDN 433
395	-----GSPKPTFLVPLLTHPSSGSDN 433
396	-----GSPKPTFLVPLLTHPSSGSDN 433
397	-----GSPKPTFLVPLLTHPSSGSDN 433
398	-----GSPKPTFLVPLLTHPSSGSDN 433
399	-----GSPKPTFLVPLLTHPSSGSDN 433
400	-----GSPKPTFLVPLLTHPSSGSDN 433
401	-----GSPKPTFLVPLLTHPSSGSDN 433
402	-----GSPKPTFLVPLLTHPSSGSDN 433
403	-----GSPKPTFLVPLLTHPSSGSDN 433
404	-----GSPKPTFLVPLLTHPSSGSDN 433
405	-----GSPKPTFLVPLLTHPSSGSDN 433
406	-----GSPKPTFLVPLLTHPSSGSDN 433
407	-----GSPKPTFLVPLLTHPSSGSDN 433
408	-----GSPKPTFLVPLLTHPSSGSDN 433
409	-----GSPKPTFLVPLLTHPSSGSDN 433
410	-----GSPKPTFLVPLLTHPSSGSDN 433
411	-----GSPKPTFLVPLLTHPSSGSDN 433
412	-----GSPKPTFLVPLLTHPSSGSDN 433
413	-----GSPKPTFLVPLLTHPSSGSDN 433
414	-----GSPKPTFLVPLLTHPSSGSDN 433
415	-----GSPKPTFLVPLLTHPSSGSDN 433
416	-----GSPKPTFLVPLLTHPSSGSDN 433
417	-----GSPKPTFLVPLLTHPSSGSDN 433
418	-----GSPKPTFLVPLLTHPSSGSDN 433
419	-----GSPKPTFLVPLLTHPSSGSDN 433
420	-----GSPKPTFLVPLLTHPSSGSDN 433
421	-----GSPKPTFLVPLLTHPSSGSDN 433
422	-----GSPKPTFLVPLLTHPSSGSDN 433
423	-----GSPKPTFLVPLLTHPSSGSDN 433
424	-----GSPKPTFLVPLLTHPSSGSDN 433
425	-----GSPKPTFLVPLLTHPSSGSDN 433
426	-----GSPKPTFLVPLLTHPSSGSDN 433
427	-----GSPKPTFLVPLLTHPSSGSDN 433
428	-----GSPKPTFLVPLLTHPSSGSDN 433
429	-----GSPKPTFLVPLLTHPSSGSDN 433
430	-----GSPKPTFLVPLLTHPSSGSDN 433
431	-----GSPKPTFLVPLLTHPSSGSDN 433
432	-----GSPKPTFLVPLLTHPSSGSDN 433
433	-----GSPKPTFLVPLLTHPSSGSDN 433
434	-----GSPKPTFLVPLLTHPSSGSDN 433
435	-----GSPKPTFLVPLLTHPSSGSDN 433
436	-----GSPKPTFLVPLLTHPSSGSDN 433
437	-----GSPKPTFLVPLLTHPSSGSDN 433
438	-----GSPKPTFLVPLLTHPSSGSDN 433
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445	-----GSPKPTFLVPLLTHPSSGSDN 433
446	-----GSPKPTFLVPLLTHPSSGSDN 433
447	-----GSPKPTFLVPLLTHPSSGSDN 433
448	-----GSPKPTFLVPLLTHPSSGSDN 433
449	-----GSPKPTFLVPLLTHPSSGSDN 433
450	-----GSPKPTFLVPLLTHPSSGSDN 433
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682	-----GSPKPTFLVPLLTHPSSGSDN 433
683	-----GSPKPTFLVPLLTHPSSGSDN 433

Matches	113;	Conservative	49;	Mismatches	164;	Indels	28;	Gaps
Y	1	MSSCSGLSRVLYAVATLVSASSPCPQAWGPGVQYOPGRSYVKLCGPVTAGDPYSWF	60					
b	1	MAASVPWACCAVLAaaaAAYTOKHSPQE-	-APHVQYERLTGTDVLPCTGASMDAAVTWR	58				
Y	61	RDGEPKLLQGPDSLGHEVLQAQDSTDEGTYCQTLOG-	-ALGTVTLQLGYPPARPVTS	119				
b	59	VNGTD--LAPDLNGSOLIIRSLRSHGSGLYACFHRSWHLRHQVLIHVGULPPREPVLS	115					
Y	120	CQADAY-ENFSCTWPSPSQLGLPRLYRILSYRKTVLGAQSRRSPSTGPWPCQFDLGA	178					
b	116	CRSTYPKFCYSPWHLs---AFI-YIPNTFNVTVLHSSKM-----MVCKDPAIKN	162					
Y	179	RCVYHGAEFWs-QYRINTEVNPLGASTRRLDVSLSQSLRDPDPOGLRVESYPGYPRRL	236					
b	163	RCHTRYMHLFESTIKYKVSLSVSNALGHNTATIIFDEFITVKDPDENVVARPVPNSNPRRL	222					
Y	237	RASHTYPASWPQCOPPHFLKFRILQYRPAQHPAWSTVEPA	GLEEVITDAVAGLPHAVRVA	295				
b	223	EVTWQTPSWPDPEFSPFLKFYLRYPLTLDWQHVELSNGTAHTITDAYAGKEYIIQAVY	282					
Y	296	RDFLDAGTMSTWSPEANGTPSTGTIPAWGQHLOTHPEVEQVDSPAPPFRPS	349					
b	283	KD-NEIGTWSDWSVAAHATPWTEE-PRHITTERQ--APETTTSTTSSLAPPPT	331					
RESULT 3								
D	IL6A_RAT	STANDARD;	PRT;	462 AA.				
C	P2273;							
T	01-AUG-1991	(Rel. 19, Created)						
T	01-FEB-1995	(Rel. 31, Last sequence update)						
T	16-OCT-2001	(Rel. 40, Last annotation update)						
E	Interleukin-6 receptor alpha chain precursor	(IL-6R-alpha) (IL-6R 1).						
N	IL6R.							
S	Rattus norvegicus (Rat).							
C	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
C	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.							
N	NCBI_TaxID=10116;							
N	[1]							
P	SEQUENCE FROM N.A.							
C	STRAIN=Fischer 344; TISSUE=Liver;							
X	MEDLINE=91060002; PubMed=2174054;							
X	Baumann M., Baumann H., Fey G.H.,							
X	*Molecular cloning, characterization and functional expression of the rat liver interleukin 6 receptor ".							
T	J. Biol. Chem. 265:19853-19862(1990).							
T	[2]							
P	IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.							
A	Gibson T.;							
A	Unpublished observations (FEB-1995).							
C	-1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6							
C	WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL							
C	ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY							
C	LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE							
C	-1- SUBUNIT: HEXAMER OF 2 IL6L ALPHA AND 2 IL6ST (BY							
C	SIMILARITY).							
C	-1- SUBCELLULAR LOCATION: Type I membrane protein.							
C	-1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE							
C	the European Bioinformatics Institute. There are no restrictions on its							
C	use by non-profit institutions as long as its content is in no way							
C	modified and this statement is not removed, usage by and for commercial							
C	entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to licensed@isb-sib.ch).							

RESULT 4

CNTFR_HUMAN	STANDARD;	PRT;	372 AA.
ID P26592; AC ;			
DT 01-AUG-1992 (Rel. 23, Created)			
DT 01-FEB-1996 (Rel. 33, Last sequence update)			
DE Ciliary neurotrophic factor receptor alpha precursor (CNTFR alpha).			
GN CNTFR.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;			
OX NCBI_TaxID=9006;			
RN [1]	SEQUENCE FROM N.A.		
RX MEDLINE-91289158; PubMed=1648265;			
RX Davis S., Aldrich T.H., Valenzuela D.M., Wong V., Furth M.E.,			
RX Squinto S.P., Yancopoulos G.D.;			
RX "The receptor for ciliary neurotrophic factor.",			
RX Science 253:59-63(1991).			
RN [2]	SEQUENCE FROM N.A.		
RX MEDLINE-95253367; PubMed=7774913;			
RX Valenzuela D.M., Rojas E., Beau M.M., Espinosa R.,			
RX Brannan C.J., McCullain J., Maslakowski P., IP N.Y., Copeland N.G.,			
RX Jenkins N.A., Yancopoulos G.D.;			
RX Genomic organization and chromosomal localization of the human and			
RX mouse genes encoding the alpha receptor component for ciliary			
RX neurotrophic factor.",			
RX Genes 25:157-163(1995).			
RX [-] FUNCTION: BINDS TO CNTF (GPA). THE ALPHA CHAIN PROVIDES THE			
RX RECEPTOR SPECIFICITY.			
RX [-] SUBUNIT: HETERTRIMER OF THE ALPHA CHAIN, LIFR AND GP130.			
RX [-] SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.			
RX [-] TISSUE SPECIFICITY: NERVOUS SYSTEM AND SKELETAL MUSCLE.			
RX [-] SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
RX [-] SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.			
RX [-] SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
TC This SWISS-PROT entry is copyright. It is produced through a collaboration			
TC between the Swiss Institute of Bioinformatics and the EMBL outstation -			
TC the European Bioinformatics Institute. There are no restrictions on its			
TC use by non-profit institutions as long as its content is in no way			
TC modified and this statement is not removed. Usage by and for commercial			
TC entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
IC EMBL; M73238; AAA3577.1; .			
IC EMBL; L38052; AAA91337.1; JOINED.			
IC EMBL; L38053; AAA91337.1; JOINED.			
IC PIR; A40854; UHUCN.			
IC Genew; HGNC:2170; CNTFR.			
IC MIM: 118946; .			
IC InterPro; IPR002996; CRIA.			
IC InterPro; IPR03961; FN_III.			
IC InterPro; IPR003530; Hemipopoptn_L_F3.			
IC InterPro; IPR003006; Ig_MHC.			
IC InterPro; IPR03598; Ig_c2.			
PFam; PF00041; fn3; 1.			
PFam; PF00047; ig; 1.			
SMART; SM00060; FN3; 1.			
SMART; SM00408; IgC2; 1.			
PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.			
Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.			
SIGNAL 1 20 POTENTIAL.			
CHAIN 21 342 CILIARY NEUROTROPHIC FACTOR RECEPTOR			
ALPHA.			
PROPEP 343 372 REMOVED IN MATURE FORM (POTENTIAL).			
DOMAIN 39 96 IG-LIKE C2-TYPE DOMAIN.			
FIBRONECTIN TYPE-III.			
DISULFID 46 302 POTENTIAL.			
CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).			

LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE REACTIONS AND HEMATOPOESIS.

-!- FUNCTION: LOW CONCENTRATION OF A SOLUBLE FORM OF INTERLEUKIN-6

CC RECEPTOR ACTS AS AN AGONIST OF IL-6 ACTIVITY.

CC -!- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R ALPHA AND 2 IL6ST.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM).

CC SECRETED (SHORT FORM).

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -!- TISSUE SPECIFICITY: THE SHORT FORM IS EXPRESSED IN PERIPHERAL BLOOD MONONUCLEAR CELLS AND weakLY FOUND IN URINE AND SERUM.

CC -!- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE N-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.

CC -!- PTM: A SHORT SOLUBLE FORM MAY ALSO BE RELEASED FROM THE MEMBRANE BY PROTEOLYSIS.

CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -!- DATABASE: NAME-PROW: NOTE=CD guide CD126 entry;
www="http://www.ncbi.nlm.nih.gov/prow/cd/cd126.htm".

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CC EMBL: X12830; CAA31312_1; .

CC EMBL: S5B298; CAA41231_1; .

CC EMBL: S72848; AAC50635_1; .

CC PIR: A41242; A41242.

CC PIR: S14621; S14621.

CC PIR: S17468; S17468.

CC PIR: JU0080; JU0080.

CC PIR: JU0080; JU0080.

CC Genew; HGNC:6019; IL6R.

CC MIM: 147880; .

CC InterPro; IPR002996; CRIA.

CC InterPro; IPR003961; FN_III_1.

CC InterPro; IPR003520; Hemtopoptn_L_F3.

CC InterPro; IPR003066; Ig_MHC.

CC InterPro; IPR003538; Ig_c2.

CC Pfam; PF00041; fn3_1.

CC Pfam; PF00047; Ig_1.

CC SMART; SM00050; FN3_1.

CC PROSITE; PS01354; HEMATopo_REC_L_F3; 1.

KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat; IG-LIKE C2-TYPE DOMAIN; Signal.

FT SIGNAL_1 19

FT CHAIN_1 19

INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.

FT DOMAIN_1 20

EXTRACELLULAR (POTENTIAL).

FT DOMAIN_1 365

POTENTIAL.

FT DOMAIN_1 387

CYTOPLASMIC (POTENTIAL).

FT DOMAIN_1 40

IG-LIKE C2-TYPE DOMAIN.

FT DISULFID_1 103

Alterative splicing; Signal.

FT DISULFID_1 193

DISULFID_1 20

DISULFID_1 365

DISULFID_1 386

DISULFID_1 468

DISULFID_1 96

DISULFID_1 132

DISULFID_1 176

DISULFID_1 55

CARBOHYD_1 93

CARBOHYD_1 93

CARBOHYD_1 221

CARBOHYD_1 221

VARSPLIC_1 356

VARSPLIC_1 365

MUTAGEN_1 132

MUTAGEN_1 134

MUTAGEN_1 140

MUTAGEN_1 153

MUTAGEN_1 165

MUTAGEN_1 174

MUTAGEN_1 176

MUTAGEN_1 184

MUTAGEN_1 190

MUTAGEN_1 193

MUTAGEN_1 211

MUTAGEN_1 217

MUTAGEN_1 232

MUTAGEN_1 233

MUTAGEN_1 254

MUTAGEN_1 277

MUTAGEN_1 278

MUTAGEN_1 279

MUTAGEN_1 280

MUTAGEN_1 281

MUTAGEN_1 285

MUTAGEN_1 291

MUTAGEN_1 293

MUTAGEN_1 468 AA: 515947 MW: 62AA239FA14FB88 CRC64;

Query Match 15.8%; Score 360; DB 1; Length 468;

Best Local Similarity 28.4%; Pred. No. 6 8e-18;

Matches 129; Conservative 57; Mismatches 196; Indels 72; Gaps 19;

QY 1 MSSSCG1SRLVYAVATLVASSSPCPQAWGPSPVQGPGRSVKLCPGVTAGD--PVS 58

Db 2 LAVGCALLAALLAAGPAAL--APRRCPCPQEVARGVPLGPDSVTLTPGPVEPEDNATVH 59

QY 59 WFRDGEPKLQGPD-----SGLGHFLVLAQADSTDEGTYCQTLDGALGTETVTLG 110

Db 60 W-----VLRKPAAGSIPSRSWGMGRILLRSVQLHSQNYSCYRA GRPACTVHLVD 111

QY 111 YPPARPVSC-QADYENFSCTWSPSQI SGLPITRLTSYRKTKTVLGADSQRSPSTG-PW 168

Db 112 VPPEEPQLCFRKSPLSNVCEMGPRSTSLL-----KAVLYFKFQNSPAEDQE 163

QY 169 PC---PQDPLGAACRYVHGAEPWSQIVINVENPIIGAS-TRLDLSQLSLRPDPQG 223

Db 164 PCYSQSEQKESQKCOLAEVEGDS--SFYTMSCVASSYVSFKSTQTDFGCGTLQDPAN 221

QY 224 LRVESVPGYPRRLRASWTPASWPQCPQPHFLKERLQYRPAQHPAWSYEPAGLEE--VIT 281

Db 222 ITVTAVANPRNLSVTNDPHSHN-S-SSTYRLRELYTAERSKTFTWVKDLQHHCVTH 280

QY 282 DAVAGLPHAVRYSARDIFLDAQTWTWSPEAWGTPSTGTPKEIPAWGGLHTOPEVEPQD 341

Db 281 DAWSGLRHVQLRAQEEFGQEWSETEAMGTPTWES-----RSPPAENEVS 328

QY 342 SPAPPRLPQLPHPLRHDSDTEQVAV---LASLGTLISFLGLIVAAALG----- 388

Db 329 TPQMAQLTINKDDNNIL-FRDSANATSFLVQDSSSVPLFEL-VAGGSIAFGTLCLIAVL 386

QY 389 ----LW-LRLRGKGDKSPKPGLFLASVLPVDRP 417

Db 387 RFKTKTWKLRALEKGTSMSHPPYTSLGQLVPERPRP 420

FT

IL6A_PIG STANDARD; PRT; 467 AA.

ID IL6A_PIG
AC A018796;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1).
DN IL6R
OS sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TAXID:9823;
RN [1]
RN SEQUENCE FROM N.A.
RP RA Morris K.R.; Strom A.D.G.;
RA "Cloning and expression of biologically active porcine IL-6 receptor."
RT RT
RL RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN RN SEQUENCE OF 123-186 FROM N.A.
RC RC TISSUE-LIVER;
RA RA Klir J.J.; Matteri R.L.;
RL RL "Partial cDNA sequence of porcine interleukin 6 receptor.";
Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC CC - FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL ACTIVATION MAY ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE REACTIONS AND HEMATOPOIESIS.
CC CC - SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY SIMILARITY).
CC CC - TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC CC - DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC CC - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC CC - SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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CC CC DR AF147881; AAF73109_1; -;
DR AF015116; AAB76916_1; -;
DR IPR02996; CRIA.
DR IPR03961; FN_III.
DR IPR03530; Hemocoptoptn_L_F3.
DR IPR03006; Ig_MHC.
DR IPR03598; Ig_c2.
DR PF00041; fn3; 19.
DR PF00047; iq; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01354; HEMATopo_REC_L_F3; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 467 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 366 386 POTENTIAL.
FT DOMAIN 387 467 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 25 193 BY SIMILARITY.
FT DISULFID 47 96 BY SIMILARITY.
FT DISULFID 121 132 BY SIMILARITY.
FT DISULFID 165 176 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 467 AA; 51066 MW; A2B0B884FF21C502 CRC64;

Query Match Score 326.5; DB 1; Length 467;
Best Local Similarity 28.2%; Pred. No. 1, 4e-15;
Matches 129; Conservative 56; Mismatches 203; Indels 69; Gaps 20;

QY 12 LYAVATAVASSSSPCP-QANGPPG-----YQYOPGRSVKLCPGYTAGD-PVSW 59
Db 1 MLAVGGALLTALLAAGMIALAPRGCSKLEYAQDVLSLPGASVTLCPGGPGDNTAHW 60

QY 60 FR----DGEPKLQGPDGLGHELYLAQDSTDGEYTCOTLDGAIGGTFLQLGYAPP 115
Db 61 VLRLNOVTGSP----DGRPAGYGRRLJLKSVOYLSGSNYSKO-DGVYAGSYRLVDPAPPEE 116

QY 116 PVVSC-QADDYENFSCTWSPSQISGLPTRYLTYSRKKKTVLGADSQRSP-STGPWNICPQD 173
Db 117 PQLSCRKSPSLSNVGCEWRP-----RSPPSPPTKAVLLVRFKONSPVVEDFOEC-QY 167

QY 174 PLGAAR-CVYHGAEEFWSOYRI-NYTEVNPLGA-STRLLDVSLSLRLPDPQGLREV 229
Db 168 SLEAQREFFCOLAVPDEDNSFHIVTLCVANSQSSTPQIFEGYGLQDPDPVNITVSAV 227

QY 230 PGYPRURASWTYPAWSWCOPQPHFLKFRLQYRPAQHPAWSVEPAGEE-VITDAVAGL 287
Db 228 DRNPNTPLSVTWDQDPWNSY-FYRLQFELRYAERSKTFTWVKCLOHHTIHDSWGM 286

QY 288 PHAVRYSARDFLDAGTWSTWSPEAWGTPST---GTPKEPLPAWGGLHTOPEVEPPVYDSP 343
Db 287 RHVVQLQRAEEFGHGLWSESOEVIGIPWTESRSSPAETEPLSQTQAPTYNEDDEISSK 346

QY 344 APPRPSLQPHPRLLDHDSDVEQAVAILASGLISFLGLVAGALGWLRLRGG----K 398
Db 347 ESANATSLP---VQDASVPLPFTLVAGGSLAFGTL---LCIGIILRFKKTGQLQALK 398

QY 399 DGS-----PKPGLFLASVLPVDRPGAPN 421
Db 399 EGKTNMHPYPSLQLVPERPKSTPVIPVPLSPVSN 435

RESULT 8
PRLR_MELGA
ID PRLR_MELGA STANDARD; PRT; 831 AA.
AC Q91094; Q91091; Q91092;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (TPRLR).
GN PRLR.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_TAXID:9103;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE-Kidney;
RX MEDLINE=97057891; PubMed=8302221;
RA Zhou J.F., Zadworny D., Gremene D., Kuhnlein U.;
RT Molecular cloning, tissue distribution, and expression of the prolactin receptor during various reproductive states in Meleagris gallopavo.;
RT Biol. Reprod. 55:1081-1090(1996).
RN SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RP TISSUE-Ovary;
RC Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
RA Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
RL This IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC - FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC - SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC DT 15-JUL-1998 (Rel. 36, Last annotation update)

CC DE Prolectin receptor precursor (PRL-R).

CC GN PRLR.

CC OS Columba livia (Domestic pigeon).

CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.

CC OC NCBI_TaxID=8932;

CC RN [1]

CC RN SEQUENCE FROM N.A.

DR RP CROPSAC;

DR RC TISSUE=CROPSAC;

DR RX MEDLINE=9423267; PubMed=7516866;

DR RA Chen X.; Horserman N.D.;

DR RT "Cloning, expression, and mutational analysis of the pigeon prolectin receptor.";

DR RL Endocrinology 135:269-276(1994);

DR CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLECTIN.

DR CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

DR CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

DR CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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FT DR EMBB; U07694; AAA20646; 1; -.

FT DR HSSP; P16471; 1BP3.

FT DR InterPro; IPRO0396; CRIA.

FT DR InterPro; IPRO03528; Hemopoptn_L_F1.

FT DR PFAM; PF00041; fn3; 4.

DR SMART; SM00060; FN3; 3.

DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.

FT SIGNAL 1 23

FT CHAIN 24

FT DOMAIN 24 831

FT PROLACTIN RECEPTOR.

FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 439 438

FT POTENTIAL.

FT DOMAIN 460 459

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 831

FT FIBRONECTIN TYPE-III 1.

FT DOMAIN 123 122

FT FIBRONECTIN TYPE-III 2.

FT DOMAIN 228 225

FT FIBRONECTIN TYPE-III 3.

FT DOMAIN 326 325

FT FIBRONECTIN TYPE-III 4.

FT DISULFID 36 46

FT BY SIMILARITY.

FT CARBOHYD 91 91

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 100 100

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 112 112

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 132 132

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 262 262

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 303 303

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 315 315

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 335 335

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQ SEQUENCE 831 AA; 94394 MW; 22091320F77FAC1 CRC64;

Query Match 10.3%; Score 234; DB 1; Length 831;

Best Local Similarity 29.0%; Pred. No. 6.8e-09;

Matches 80; Conservative 40; Mismatches 106; Indels 50; Gaps 15;

QY 113 PARP-VVSCQAADYENFCTWSQISQLPTRYLTSYRKTKTVLGADSQRSPSTGPWPCP 1.71

Db 28 PGKPKIICRSLEKEETSCWWPKGSDGLPTNLYFLYSK----DSSEEKI----YECP 76

QY 172 Q-DPLGARCVYHG--AEFWQSQRINVTEVNPLGAST---RLLDVSQSLRFDPQQGLR 225

Db 77 DYTTSGPNSCYFRNNTYNTATNEIGNSNSDPQYVDT -SIVPGSPVNLT 1.34

QY 226 VESVPGVPR----LRSWTPASWPCOPHFLKSRQYPAQHPAWSTVEPAGLE- 278

Db 135 LET----QRYANIMYLWAKNSPPLLADASSMHLHYELRKPEEEWEIW-PVGVQTQ 188

QY 279 -VITDAVGLPHAVRVSARDFLAGTMWTSWEAWGTPSTGTIPKEIPANGOLHTQEVE 337

Db 189 CKNRLNAGMRVVQV -RCMLDPGENSESSERRILLISGSPPEKPTIKCRS-PEKE 245

QY 338 -----PQVDSPAPPRLSPQPHPRLLDHRDSEVEQ 366

Db 246 TFTCWWKPGLDGGHPTNYT----LLYSKEECEEQV 275

QY RESULT 9

PRTR_COILI TD PRTR_COILI STANDARD; PRT; 830 AA.

AC Q90374; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DR RN SEQUENCE FROM N.A.

DR RC TISSUE=CROPSAC;

DR RX MEDLINE=9423267; PubMed=7516866;

DR RA Chen X.; Horserman N.D.;

DR RT "Cloning, expression, and mutational analysis of the pigeon prolectin receptor.";

DR RL Endocrinology 135:269-276(1994);

DR CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLECTIN.

DR CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

DR CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

DR CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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DR DR EMBB; U07694; AAA20646; 1; -.

DR DR HSSP; P16471; 1BP3.

DR DR InterPro; IPRO0396; CRIA.

DR DR InterPro; IPRO03528; Hemopoptn_L_F1.

DR DR PFAM; PF00041; fn3; 4.

DR SMART; SM00060; FN3; 3.

DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.

FT SIGNAL 1 23

FT CHAIN 24

FT DOMAIN 24 831

FT PROLACTIN RECEPTOR.

FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 439 438

FT POTENTIAL.

FT DOMAIN 460 459

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 831

FT FIBRONECTIN TYPE-III 1.

FT DOMAIN 123 122

FT FIBRONECTIN TYPE-III 2.

FT DOMAIN 228 225

FT FIBRONECTIN TYPE-III 3.

FT DOMAIN 326 325

FT FIBRONECTIN TYPE-III 4.

FT DISULFID 36 46

FT BY SIMILARITY.

FT CARBOHYD 91 91

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 100 100

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 112 112

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 132 132

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 262 262

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 303 303

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 315 315

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 335 335

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQ SEQUENCE 831 AA; 94394 MW; 22091320F77FAC1 CRC64;

Query Match 9.0%; Score 221; DB 1; Length 830;

Best Local Similarity 29.0%; Pred. No. 5.2e-08;

Matches 67; Conservative 36; Mismatches 90; Indels 38; Gaps 12;

QY 111 YPPARPYVSCQADYENFCTWSQISQLPTRYLTSYRKTKTVLGADSQRSPSTGPWPC 1.70

Db 27 YPGPKIICRSLEKEETSCWWPKGSDGLPTNLYFLYSK----DSEEKI----YEC 75

QY 171 PDPL-GAARCYY -HGAEFWSQYRINTENPLGAST---RILDVLSQSLRDPQQGL 224

Db 76 EDYGMSSPNSCYFDKNHTNPRTYNTMAMEIGNSNSDPQYVDTI-SIVQDPAPVNL 1.33

QY 225 RVEVSPGYPRRLRASWY -PASWPQCPD-----HFLKFRLQYRPAQHPANSTVEPAGL 276

Db 134 SLET-----RTSASTYLAKWSPPELAQVTSNSHVRRLPEEKSEWETVS-VGV 186
 ID PRLR_CHICK
 AC 004594;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Prolactin receptor precursor (PRL-R) (CBRLP).
 GN Gallus gallus (Chicken).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galiiformes; Phasianidae; Phasianinae; Gallus.
 OC NCBI_TaxID=9031;
 OX RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAN=White leghorn; TISSUE=Kidney;
 RX MEDLINE93075122; PubMed=1445292;
 RA Tanaka M., Maeda K., Okubo T., Nakashima K.; RT "Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence.";
 RL Biochem. Biophys. Res. Commun. 188:490-496 (1992).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC DR EMBL: D13154; BAA02439.1; -.
 DR PIR: JQ1655; JQ1655.
 DR HSSP: P16471; IBP3.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003528; Hemocoptoptn_L_F1.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 831
 FT DOMAIN 24 438
 FT TRANSMEM 439 459
 FT DOMAIN 460 831
 FT DOMAIN 25 122
 FT DOMAIN 123 225
 FT DOMAIN 228 325
 FT DOMAIN 326 428
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 262 262
 FT CARBOHYD 303 303
 FT CARBOHYD 315 315
 PT CARBOHYD 335 831 AA; 94102 MW; 1C4E7591DCADBE9 CRC64;
 SQ SEQUENCE 9.4%; Score 214; DB 1; Length 831;
 Query Match Best Local Similarity 27.5%; Pred. No. 1.6e-07;
 Matches 76; Conservative 42; Mismatches 108; Indels 50; Gaps 15;

RESULT 10
 PRLR_CHICK STANDARD; PRT; 831 AA.
 QY 277 EE--VITDAAGLPHAVRYVARDLFAGITWSTWSAEAGCTPSTGTIPKEEP 325
 DB 187 QTQYKVNRQAGVKTvvQV--RCVLDIGENSESSERLHIIPINGESPPERP 235
 FT PARP-VVSCQQADYENINFSCWVTPSQLSGLPTRFLTYRKTKVGLGDSQRSPSTGWPCP 171
 ID PRLR_CHICK
 AC 004594;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Prolactin receptor precursor (PRL-R) (CBRLP).
 GN Gallus gallus (Chicken).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galiiformes; Phasianidae; Phasianinae; Gallus.
 OC NCBI_TaxID=9031;
 OX RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAN=White leghorn; TISSUE=Kidney;
 RX MEDLINE93075122; PubMed=1445292;
 RA Tanaka M., Maeda K., Okubo T., Nakashima K.; RT "Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence.";
 RL Biochem. Biophys. Res. Commun. 188:490-496 (1992).
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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 CC DR EMBL: D13154; BAA02439.1; -.
 DR PIR: JQ1655; JQ1655.
 DR HSSP: P16471; IBP3.
 DR InterPro: IPR002996; CR1A.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003528; Hemocoptoptn_L_F1.
 DR Pfam: PF00041; fn3; 4.
 DR SMART: SM00060; FN3; 3.
 DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
 FT SIGNAL 1 23
 FT CHAIN 24 831
 FT DOMAIN 24 438
 FT TRANSMEM 439 459
 FT DOMAIN 460 831
 FT DOMAIN 25 122
 FT DOMAIN 123 225
 FT DOMAIN 228 325
 FT DOMAIN 326 428
 FT DISULFID 36 46
 FT DISULFID 75 86
 FT CARBOHYD 59 59
 FT CARBOHYD 91 91
 FT CARBOHYD 100 100
 FT CARBOHYD 112 112
 FT CARBOHYD 132 132
 FT CARBOHYD 262 262
 FT CARBOHYD 303 303
 FT CARBOHYD 315 315
 PT CARBOHYD 335 831 AA; 94102 MW; 1C4E7591DCADBE9 CRC64;
 SQ SEQUENCE 9.4%; Score 214; DB 1; Length 831;
 Query Match Best Local Similarity 27.5%; Pred. No. 1.6e-07;
 Matches 76; Conservative 42; Mismatches 108; Indels 50; Gaps 15;

RESULT 11
 PRLR_SHEEP
 ID PRLR_SHEEP STANDARD; PRT; 581 AA.
 AC 046561; P79205; 046574; P79203; 046569;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Prolactin receptor precursor (PRL-R) (OPR).
 GN PRLR.
 OS Ovis aries (Sheep).
 OC Bovidae; Metacea; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPlicing.
 RC TISSUE=Liver, and Mammary gland;
 RX MEDLINE=9801468; PubMed=9143303;
 RP SPECIFICITY.
 RC STRAIN=Scottish blackface; TISSUE=Anterior pituitary;
 RX MEDLINE=99049302; PubMed=983246;
 RA Tortonese D.J., Brooks J., Ingleton P.M., McNeilly A.S.;
 RA RT "Detection of prolactin receptor gene expression in the sheep pituitary gland and visualization of the specific translation of the signal in gonadotropins.";
 RT RL Endocrinology 139:5215-5223 (1998).
 RN [13]
 RP SEQUENCE OF 147-302 FROM N.A., ALTERNATIVE SPlicing, AND TISSUE SPECIFICITY.
 RC TISSUE=Corpus luteum, and Fetal liver;
 RA Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.;
 RT RT "Two forms of the prolactin receptor messenger ribonucleic acid are present in ovine fetal liver and adult ovary.";
 RT RL Endocrine 3:291-295 (1995).
 CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone prolactin.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 3 isoforms; 1/long/L-OPR (shown here),
 CC -!-

2/short/S-QPR and 3/soluble; are produced by alternative splicing.

CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined; liver, pituitary, adrenal gland, ovary and fetal liver.

CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC DR EMBL; AF041257; AAB96795_1;

CC DR EMBL; AF041977; AAB96920_1;

CC DR EMBL; AF041979; AAB97082_1;

CC DR EMBL; AF042358; AAB97744_1;

CC DR EMBL; AF042358; AAB97745_1;

CC DR EMBL; AF041978; AAB97965_1;

CC DR EMBL; Y10578; CAA71597_1;

CC DR EMBL; Y10808; CAQ71166_1;

CC DR HSSP; P14787; IAN3;

CC DR InterPro; IPR002996; CRIA.

CC DR InterPro; IPR003961; FN_III_1.

CC DR InterPro; IPR003528; Hemopoptn_L_F1.

CC DR Pfam; PF00041; fn3_2;

CC DR SMART; SM00060; FN4_2;

CC DR PROSITE; PS01352; HEMATopo_REC_L_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;

KW Alternative splicing.

FT SIGNAL 1 24 POTENTIAL.

FT DOMAIN 25 581 PROLACTIN RECEPTOR.

FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 238 258 POTENTIAL.

FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.

FT DOMAIN 123 227 FIBRONECTIN TYPE-III 2.

FT DISULFID 36 46 BY SIMILARITY.

FT DISULFID 75 86 BY SIMILARITY.

FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPLIC 24 66 GQSPPEKPKRSPGKFETCWWEPADGGIPLPTNTUTYRK > ASLYVPGKGCKCSVCYTMAYPVGIGPLHMYLVCY DOYLLVTS (IN ISOFORM 3).

FT VARSPLIC 67 581 MISSING (IN ISOFORM 3).

FT VARSPLIC 286 296 KGKESEELRL > ISQPSRLYSVF (IN ISOFORM 2)

FT VARSPLIC 297 581 MISSING (IN ISOFORM 2).

FT CONFLICT 281 281 I > V (IN REF. 1; AAB97743//AAB97744),

FT CONFLICT 387 387 E > K (IN REF. 2).

SQ SEQUENCE 581 AA; 65235 MW; EC5344DE538837/A0 CRC64;

Query Match 9.28; Score 209.5; DB 1; Length 581;
Best Local Similarity 26.88; Pred. No. 2.e-07;
Matches 61; Conservative 36; Mismatches 94; Indels 37; Gaps 10;

QY 112 PDPAP-VVSQADYENFSCTIVSPSQISGLPLPRTYLTSYRKVVLGADSQRSPSTGWPC 170

DR 27 PPEPKLUJKCRPKGEFTCWNPEGADGGLPNNTYLRKE-----GETIHEC 75

QY 171 PDPPLGALARCVYHGAEEF --WQYQIRNTEVNPLG-ASTRLDVSLSIQLRDPQQPQLRV 226

DR 76 PDYKTKGPNSCYESKSKRTSIWMMVITSAINQMGTSSSDPYVDTYIVEPPVNLT 135

QY 227 ESYPGYPRR--LRSATYP-----ASWPQCQFHLLFKRLQYRPQAHPAWT-VEPAGLE 277

DR 136 EUKHPEDRPKPYWIKWSPPLTDVKSGW-----FSIQEIRKPAETDWTHFAPKLQ 190

QY 278 EYITDAYAGLPHAVYRSARDFLDAGTWSTWSEAWGTPSTGTIPKEP 325

DR 191 LKIFNLYPGOKLYVQTRCKP-DHGTYSEWSSE-----SFTQIPNDFF 231

RESULT 12
PRLR_BOVIN STANDARD; PRT; 581 AA.
ID Q2B17_2; O18880; 046591;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prolactin receptor precursor (PRLR).
GN PRLR.
OS Bos taurus (Bovine).
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos.
OC NCBI_TaxID:9913;
OX [1]
RN RP SEQUENCE FROM N.A. (LONG ISOFORM).
RC TISSUE=Endometrium;
MEDLINE=932465019; PubMed=1338725;
RA Scott P.; Kessler M.A.; Schulz L.A.; RT Molecular cloning of the bovine prolactin receptor and distribution of prolactin and growth hormone receptor transcripts in fetal and utero-placental tissues.";
RL Mol. Cell. Endocrinol. 89:47-58 (1992).
RN [2]
RP SEQUENCE FROM N.A. (SHORT ISOFORM), AND TISSUE SPECIFICITY.
RC TISSUE=Endometrium;
MEDLINE=97375450; PubMed=9231767;
RA Schuler L.A.; Nagel R.J.; Gao J.; Horseman N.D.; Kessler M.A.; RT "Prolactin receptor heterogeneity in bovine fetal and maternal tissues";
RL Endocrinology 138:3187-3194 (1997).
RN [3]
RP SEQUENCE OF 25-234 FROM N.A., AND SEQUENCE OF 25-33.
RC TISSUE=Hammary gland;
MEDLINE=95256770; PubMed=7738463;
RA Teitel A.; Staten N.R.; Creely D.P.; Kriivi G.G.; Gertler A.; RT "Extracellular domain of prolactin receptor from bovine mammary gland: expression in Escherichia coli, purification and characterization of its interaction with lactogenic hormones.";
RT Mol. Endocrinol. 14:393-403 (1995).
RN [4]
RP ALTERNATIVE SPlicing.
RA Bignon C.; Binart N.; Ormandy C.; Schuler L.A.; Kelly P.A.; Djiane J.; RT "Long and short forms of the ovine prolactin receptor: cDNA cloning and genomic analysis reveal that the two forms arise by different RT alternative splicing mechanisms in ruminants and in rodents.";
RL J. Mol. Endocrinol. 19:109-120 (1997).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
RA Bignon C.; Binart N.; Ormandy C.; Schuler L.A.; Kelly P.A.; Djiane J.; RT "Long and short forms of the ovine prolactin receptor: cDNA cloning and genomic analysis reveal that the two forms arise by different RT alternative splicing mechanisms in ruminants and in rodents.";
RL J. Mol. Endocrinol. 19:109-120 (1997).
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a short form; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined; liver, peripheral blood lymphocytes, endometrium, corpus luteum, intestine, fetal thymus, fetal spleen, fetal liver and fetal brain.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

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DR EMBL; L02543; AAA51417_1; -.
DR EMBL; AF027403; AAB8399_1; -.
DR EMBL; AF042780; AAB97748_1; -.
DR EMBL; AF042780; AAB97747_1; ALT-SEQ.


```

Db    65 SSEVL----GSGKTLTILVKEFEDAGHYTCRR----GEVLSQMLLHKNEDGIWST 114
Qy   110 ----GFPARPVSCOADYE-NFSCTWSPSQISGIPTRVLTSYKKTVLGADSQRSP 163
     | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    115 DILKKKEPENKNLVTCRANKNSGRFTCWW-----LTAISTDVNFSVKSHRGSS 162
Qy   164 STGPWPQPQDPLGAACRVHGAEPFWSYRINVTEVNPLGASTRLLDVS----- 211
     | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    163 DPGVYTGEATLSAERYKIEQEY - KKYSVQCQEDNACPTAETLPITVVVDAVHKLKYE 221
     | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy   212 -----LQSTLRPDPPQGLRYESVPGYPRRLRASWTPASWPCOPH - FLLKFRLQYRP 262
     | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    222 NYISSFFTRDIKPDPPKNLAKMP - SKTPQQVEVTWEYPDSM - STPHSYFSLTFSVQVQG 279
     | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy   263 AQHPAWSTVEPAGLEEVITDAVAGLPHAVRYSARDFELDAGWSTWS 308
     | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    280 KKKKRNTLH - - VDKTSVTVTCQKGAKVSYQARDRYNNSSSEWA 322
     | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Search completed: January 17, 2003, 19:38:22
 Job time : 18 secs

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Result No.	Score	Query Match	Length	DB ID	Description
1	2275	100.0	422	2 137891	interleukin-11 receptor alpha chain - human
2	1897	83.4	432	2 148343	C; Species: Homo sapiens (man)
3	395.5	17.4	460	2 JLO145	C; Date: 29-May-1998 #text_change 03-Dec-1999
4	39.2	17.2	372	2 I58141	C; Accession: I37891; GO1970; G01971
5	389.5	17.1	440	2 JLO144	R; Chereci, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Minviell
6	380	16.7	362	2 S60614	Blood 86, 2534-2540, 1995
7	379	16.7	372	1 UHHUCN	A; Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic
8	360	15.8	468	1 A41242	A; Reference number: I37891; MUID:95399754; PMID:7670098
9	298.5	13.1	462	1 A37986	A; Accession: I37891
10	221	9.7	830	2 I50455	A; Molecule type: mRNA
11	214	9.4	831	2 JOL655	A; Residues: 1-422 <RES>
12	204.5	9.0	581	2 I41971	A; Cross-references: EMBL:238102; NID:9995653; PIDN:CAA86224.1; PID:9995654
13	204	9.0	616	2 A30304	R; Van Leeuwen, F.
14	189	8.3	288	2 B59405	submitted to the EMBL Data Library, July 1995
15	189	8.3	376	2 A54045	A; Residues: 1-422 <VAN>
16	189	8.3	622	2 A40144	R; Van Leeuwen, F.
17	186	8.2	1265	1 A37967	A; Status: preliminary; translated from GB/EMBL/DDBJ
18	183	8.0	310	2 A29884	A; Reference number: G08959
19	183	8.0	412	2 A41070	A; Accession: G01970
20	183	8.0	610	2 A3631	A; Status: preliminary; translated from GB/EMBL/DDBJ
21	183	8.0	610	2 A36116	A; Molecule type: DNA
22	174	7.6	292	2 I77525	A; Cross-references: ENBL:U32323; NID:9975334; PIDN:AAB36491.1; PID:9975335
23	174	7.6	303	2 I77524	R; Van Leeuwen, F.
24	174	7.6	608	2 I53269	A; Status: preliminary; translated from GB/EMBL/DDBJ
25	173.5	7.6	630	2 I51086	A; Residues: 1-422 <VA2>
26	167.5	7.4	328	2 A39957	A; Cross-references: EMBL:032324; NID:9975336; PIDN:AAB36492.1; PID:9975337
27	166.5	7.3	761	1 IJHUNG	C; Genetics:
28	150	6.6	918	2 A36337	A; Introns: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 418/1
29	149.5	6.6	853	1 IUBONC	C; Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology <CRS>; F; 120-310/Domain: cytokine receptor homology <CRS>

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2275	100.0	422	2 137891	interleukin-11 receptor alpha chain - human
2	1897	83.4	432	2 148343	interleukin-11 receptor
3	395.5	17.4	460	2 JLO145	interleukin-6 receptor
4	39.2	17.2	372	2 I58141	ciliary neurotrophin receptor
5	389.5	17.1	440	2 JLO144	interleukin-6 growth promoter
6	380	16.7	362	2 S60614	growth promoting cytokine receptor
7	379	16.7	372	1 UHHUCN	ciliary neurotrophin receptor
8	360	15.8	468	1 A41242	interleukin-6 receptor
9	298.5	13.1	462	1 A37986	interleukin-6 receptor
10	221	9.7	830	2 I50455	prolactin receptor
11	214	9.4	831	2 JOL655	prolactin receptor
12	204.5	9.0	581	2 I41971	prolactin receptor
13	204	9.0	616	2 A30304	prolactin receptor
14	189	8.3	288	2 B59405	prolactin receptor
15	189	8.3	376	2 A54045	prolactin receptor
16	189	8.3	622	2 A40144	prolactin receptor
17	186	8.2	1265	1 A37967	neural cell adhesion molecule receptor
18	183	8.0	310	2 A29884	prolactin receptor
19	183	8.0	412	2 A41070	lactogen receptor
20	183	8.0	610	2 A3631	prolactin receptor
21	183	8.0	610	2 A36116	prolactin receptor
22	174	7.6	292	2 I77525	prolactin receptor
23	174	7.6	303	2 I77524	prolactin receptor
24	174	7.6	608	2 I53269	prolactin receptor
25	173.5	7.6	630	2 I51086	prolactin receptor
26	167.5	7.4	328	2 A39957	interleukin-12B receptor
27	166.5	7.3	761	1 IJHUNG	neural cell adhesion molecule receptor
28	150	6.6	918	2 A36337	membrane glycoprotein receptor
29	149.5	6.6	853	1 IUBONC	neural cell adhesion molecule receptor

QY	181	VVHGAFFWSQRINVTENVNPLGASTRLDVSLSLIRPDPGLRVESEPGYPRLRASW	240		Db	241	TYPASWRQPHFLKFRQLQYRPAQHPAWSVTEPIGLEEVITDAVLPHAVRSARDFLD	300
Db	181	VVHGAFFWSQRINVTENVNPLGASTRLDVSLSLIRPDPGLRVESEPGYPRLRASW	240					
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Db	241	TYPASWCQPHFLKFRQLQYRPAQHPAWSVTEPIGLEEVITDAVLPHAVRSARDFLD	300		Db	301	AGTWSIWSPAWGTPSTGTIPKEPAWGQOLHTQDEPDWSQGHQOLEAVQAEDSPAPRSPSLQDPRPILD	360
Qy	301	AGTWSIWSPAWGTPSTGTIPKEPAWGQOLHTQ - PEVFEQVDSPPAPRPSLQPHPRLLD	360		Qy	359	HRDSEQVAVLASIGLTSFLGLVAGALAGLWLRLRGSKDGPQKPGILAPMIPVEKLPG	418
Db	301	AGTWSIWSPAWGTPSTGTIPKEPAWGQOLHTQ - PEVFEQVDSPPAPRPSLQPHPRLLD	360		Db	361	HRDPEQVAVLASIGLTSFLGLVAGALAGLWLRLRGSKDGPQKPGILAPMIPVEKLPG	420
Qy	361	DSVEQAVLASIGLTSFLGLVAGALAGLWLRLRGSKDGPQKPGILAPMIPVEKLPG	420		Qy	419	APNL 422	
Db	361	DSVEQAVLASIGLTSFLGLVAGALAGLWLRLRGSKDGPQKPGILAPMIPVEKLPG	420		Db	421	IPNL 424	
Qy	421	NL 422						
Db	421	NL 422						
RESULT 3								
		JL0145						
		interleukin-6 receptor precursor (clone lambda 301) - mouse						
C;Species:	Mus musculus (house mouse)							
C;Date:	31-Dec-1991 #sequence_revision							
C;Accession:	JL0145; S14543							
R;Sugita, T.; Toritsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, J. Exp. Med. 171, 2001-2009, 1990								
A;Title:	Functional murine interleukin 6 receptor with the intracisternal a particle							
A;Reference number:	JL0144; MUID:90278354; PMID:2112585							
A;Accession:	JL0145							
A;Status:	nucleic acid sequence not shown							
A;Molecule type:	mRNA							
A;Residues:	1-460 <SUGO>							
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C;Date:	02-Jul-1996 #sequence_revision							
C;Accession:	I48343; S51619							
A;Title:	Bilinski, B.; Bettehausen, H.; Bettenhausen, H.; Bettehausen, B.; Bilinski, P.; Simon-Chazottes, D.; Guenet, J.L.; Gossel Dev. Biol. 166, 521-542, 1994							
A;Reference number:	I48343							
A;Accession:	I48343							
A;Status:	preliminary							
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A;Residues:	1-432 <RE3>							
A;Cross-references:	EMBL:X74953; NID:9673437; PID:CAA52908.1; PID:9673438							
EMBO J. 13, 4765-4775, 1994								
A;Title:	Cloning of a murine IL-11 receptor alpha-chain: requirement for gp130 for high A;Reference number:	S51619; MUID:95045367; PMID:7957045						
A;Accession:	S51619							
A;Status:	preliminary							
A;Molecule type:	mRNA							
A;Residues:	1-432 <HTL>							
C;Cross-references:	EMBL:U14412; NID:9576454; PID:AAA53248.1; PID:9576455							
A;Gene:	Et12/III.1							
C;Superfamily:	ciliary neurotrophic factor receptor							
C;Keywords:	cytokine receptor							
F;120-310/Domain:	cytokine receptor homology <CRS>							
Query Match								
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Db	1	MSSSCGSLRVAVATALVYASSSPCPOAWGPGPVQYGPGRSVKLCGPVTAQDPVSWF	60		Db	2	Ltvctllvallaapavalvlvs - -CRALEAVANGTVTSPGATVTLICGKEAGNVTH	59
Qy	61	RDGEPKLIQGPDSGLGHVELQADQSTDEGTYTCQTLGAGTGTQVLPQGPVRYSC 120			Qy	59	WFRDCEPKLIQGPDSGLGHVELQADQSTDEGTYTCQTLGAGTGTQVLPQGPVRYSC 117	
Db	61	RDGEPKLIQGPDSGLGHVELQADQSTDEGTYTCQTLGAGTGTQVLPQGPVRYSC 120			Db	60	WVYSGS - -QNREWTNTLVLVDQIISDGTGDCYL - SLNDHLVGTVPLLVDPVPEEK	114
Qy	121	QADYENFSCTRSPSQISCOLPTRLTSRKKTVLGADSQRSTGPMPCPOPPLGARC 180			Qy	118	VSC-QAADWENFSCTWSPQISQGLPTRYLTSYRKTVLQGADSQRSPSTGPWPWCP-QDPL	175
Db	121	QADYENFSCTRSPSQISCOLPTRLTSRKKTVLGADSQRSTGPMPCPOPPLGARC 180			Db	115	LSERKRNPLVNACEWRSSTPS-PTKAVLFKKI - - -NITNGKSDFOVPCQYSQQL	168
Qy	181	VVHGAFFWSQRINVTENVNPLGASTRLDVSLSLIRPDPGLRVESEPGYPRLRASW	240		Qy	176	GAACVYHGAEFWNSQYRI - NYTEVNPLGASTRLDV - -SLSQSLRLPQGSTRLLDV	232
Db	181	VVHGAFFWSQRINVTENVNPLGASTRLDVSLSLIRPDPGLRVESEPGYPRLRASW	240		Db	169	KFSSCQEILELEGDRVYHSLVCSKSHNEAFHSLK - MVQOPPANLVVAIPGR	227
Qy	241	TYPASWCQPHFLKFRQLQYRPAQHPAWSVTEPIGLEEVITDAVLPHAVRSARDFLD	300		Qy	233	PRURASWTPASWPCQPHFLKFRQLQYRPAQHPAWS - - -TVEPALEEVITDAVG	286
Db	241	TYPASWCQPHFLKFRQLQYRPAQHPAWSVTEPIGLEEVITDAVLPHAVRSARDFLD	300		Db	228	PRWLKVSWQHPETWD - PSYUQQLQFQRLRYR - - -PWWKSFETVLLPVVAQYQCIVHDALRG	282

Qy	287	LPHAVRSARDLFAGTWSPEAWGTPSTGTIPKEIPA---WGQLHTQPEVEPOVQDSP	343	RESULT 5
Db	283	VKHLVQVRKEEGLDGGONSEWSPEVTGPWIAE-PRTPAGLWNP---TOVSVE---DS-	335	interleukin-6 receptor precursor (clone lambda P1) - mouse
Qy	344	APPRPSLQPHPRLLDHRD---SVEQAVALW-----SLGILSFLGLVAGALALGLW--	390	C;Species: Mus musculus (house mouse)
Db	336	-----ANHEDOYESSTEATSVLAPYQESSSMSLPFFL-VAGGSIAFGLLCV	381	C;Accession: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
Qy	391	--LRLRGGKD-----GSPKPGFLASVTPVDRRGAPN 421	433	C;Accession: JL0144
Db	382	FITLRLKQRWKSEAEKESKTSPPPTSLGPLRPTFLVPLDTPHSQSDN	433	A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle
		A;Reference number: JL0144; MUID:90278354; PMID:2112585		A;Reference number: JL0144
		A;Status: nucleic acid sequence not shown		A;Status: nucleic acid sequence not shown
		A;Molecule type: mRNA		A;Molecule type: mRNA
		A;Residues: 1-440 <SOG>		A;Residues: 1-440 <SOG>
		A;Cross-references: GB:X51976; NID:953548; PID:CAA36238_1; PID:953549		C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology: immu
		C;Keywords: cytokine receptor; transmembrane protein		C;Keywords: cytokine receptor; transmembrane protein
		C;Accession: F:1-19/Domain: signal sequence #status predicted <SIG>		F:1-19/Domain: signal sequence #status predicted <SIG>
		C;Accession: F:20-44/Domain: Interleukin 6 receptor #status predicted <MAT>		F:20-44/Domain: Interleukin 6 receptor #status predicted <MAT>
		C;Accession: F:45-94/Domain: immunoglobulin homology <IMM>		F:45-94/Domain: immunoglobulin homology <IMM>
		C;Accession: F:117-306/Domain: cytokine receptor homology <CRS>		F:117-306/Domain: cytokine receptor homology <CRS>
		C;Accession: F:358-385/Domain: transmembrane #status predicted <TRA>		F:358-385/Domain: transmembrane #status predicted <TRA>
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.1%; Score 389.5; DB 2; Length 440;		A;Residues: 1-440 <SOG>
		Best Local Similarity 32.3%; Pred. No. 1.4e-18; Indels 67; Gaps 23;		C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology: immu
		Matches 135; Conservative 54; Mismatches 162;		C;Keywords: cytokine receptor; transmembrane protein
Qy	158141	158141 X51976	58	C;Accession: F:1-19/Domain: signal sequence #status predicted <SIG>
		C;Species: Rattus norvegicus (Norway rat)		F:1-19/Domain: signal sequence #status predicted <SIG>
		C;Keywords: ciliary neurotrophic factor receptor; cytokine receptor homology: immu		F:20-44/Domain: Interleukin 6 receptor #status predicted <MAT>
		C;Accession: F:45-94/Domain: immunoglobulin homology <IMM>		F:45-94/Domain: immunoglobulin homology <IMM>
		C;Accession: F:117-306/Domain: cytokine receptor homology <CRS>		F:117-306/Domain: cytokine receptor homology <CRS>
		C;Accession: F:358-385/Domain: transmembrane #status predicted <TRA>		F:358-385/Domain: transmembrane #status predicted <TRA>
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.1%; Score 389.5; DB 2; Length 440;		A;Residues: 1-440 <SOG>
		Best Local Similarity 32.3%; Pred. No. 1.4e-18; Indels 67; Gaps 23;		C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology: immu
		Matches 135; Conservative 54; Mismatches 162;		C;Keywords: cytokine receptor; transmembrane protein
Qy	1	MSSSCSCSLSRVLAVATALVASSPCPQAWGPPGVQXOPGRSVKLCCPGVTAGDPVSMF	58	Query 1 MSSSCSCSLSRVLAVATALVASSPCPQAWGPPGVQXOPGRSVKLCCPGVTAGDPVSMF - 58
Db	2	LTIVGCTLLYVLAAPAVALVLS-----CRALEAVANTVSLSPGATVTLICPGKEAAGNTVTH	59	Db 2 LTIVGCTLLYVLAAPAVALVLS-----CRALEAVANTVSLSPGATVTLICPGKEAAGNTVTH 59
Qy	59	WFDEGPKLQGPD-SGLGHELVIAQADSTDEGTYCOTLDGAJLGJTVTLQLGYPARPV 117	59	Query 59 WFDEGPKLQGPD-SGLGHELVIAQADSTDEGTYCOTLDGAJLGJTVTLQLGYPARPV 117
Db	60	WVYSGS---QNRENTIGNTNLVLRDQLSLTDGDYLCS-LNDNHLVGTPLLVDPVPEEPK 114	60	Db 60 WVYSGS---QNRENTIGNTNLVLRDQLSLTDGDYLCS-LNDNHLVGTPLLVDPVPEEPK 114
Qy	118	VSC-QAADYENFSCTWSPOISGLPTRYLTSYRKTKTVLGADSQRRSPSSTGPWPSCP-QDPL 175	118	Query 118 VSC-QAADYENFSCTWSPOISGLPTRYLTSYRKTKTVLGADSQRRSPSSTGPWPSCP-QDPL 175
Db	115	LSCFRKNPVNACIEMWRPSSTPS-PTTKAVLFARKI----NTNTGKSDEQVPCQYSQOL 168	115	Db 115 LSCFRKNPVNACIEMWRPSSTPS-PTTKAVLFARKI----NTNTGKSDEQVPCQYSQOL 168
Qy	176	GAACRCVHGAEFWQYRI-NVTEVNPLGASTRLDV--SLSQSLRDPDQGLRVEVSPYQ 232	176	Query 176 GAACRCVHGAEFWQYRI-NVTEVNPLGASTRLDV--SLSQSLRDPDQGLRVEVSPYQ 232
Db	169	KSFSCSQVTEILEGDKVYHTVSLCVANSVGSKSHNEAFHSLK-MYQDPDPAVLVVAIPER 227	169	Db 169 KSFSCSQVTEILEGDKVYHTVSLCVANSVGSKSHNEAFHSLK-MYQDPDPAVLVVAIPER 227
Qy	233	PRLRASWTPASWCPQPHFLKLKRPLQYRPAQHAWA-----TVEPAGLEEVITDAVAG 286	233	Query 233 PRLRASWTPASWCPQPHFLKLKRPLQYRPAQHAWA-----TVEPAGLEEVITDAVAG 286
Db	228	PRWLKVSNQHQPETWD-PSYLYLQQPLRYR---PVWSKKEFTVLLPVQYQCYVHDALRG 282	228	Db 228 PRWLKVSNQHQPETWD-PSYLYLQQPLRYR---PVWSKKEFTVLLPVQYQCYVHDALRG 282
Qy	287	LPHAVRVSARDFELDAGTWSTWSPEAWGTPSTGTIPKEITA---WGQLHTQPEVEPVQDVPSP 343	287	Query 287 LPHAVRVSARDFELDAGTWSTWSPEAWGTPSTGTIPKEITA---WGQLHTQPEVEPVQDVPSP 343
Db	283	VKHVVQVRGEELDQGQWSEWSPEVGTGPWIAE-PTTPAGLWNP--TQVSVE--DS- 335	283	Db 283 VKHVQVRGEELDQGQWSEWSPEVGTGPWIAE-PTTPAGLWNP--TQVSVE--DS- 335
Qy	344	APPRLPSLQHPPLRDLHD---SVEQAVALA-----SUGILSFLGVLGAGALALGLWL 391	344	Query 344 APPRLPSLQHPPLRDLHD---SVEQAVALA-----SUGILSFLGVLGAGALALGLWL 391
Db	336	-----ANHEDOYESSTEATSVLAPYQESSSMSLPTFL-VAGGSLAFLGLL 379	336	Db 336 -----ANHEDOYESSTEATSVLAPYQESSSMSLPTFL-VAGGSLAFLGLL 379
		RESULT 6		
		S60614 growth promoting activity receptor alpha precursor - chicken		C;Species: Gallus gallus (chicken)
		C;Accession: S60614 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000		C;Accession: S60614 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
		R;Heiler, S.; Finn, T.P.; Huber, J.; Nishi, R.; Geissen, M.; Pueschel, A.W.; Rohrer, A;Title: Analysis of function and expression of the chick GPA receptor (GPalpha1) su		R;Heiler, S.; Finn, T.P.; Huber, J.; Nishi, R.; Geissen, M.; Pueschel, A.W.; Rohrer, A;Title: Analysis of function and expression of the chick GPA receptor (GPalpha1) su
		A;Reference number: S60614; MUID:5401882; PMID:7671828		A;Reference number: S60614; MUID:5401882; PMID:7671828
		A;Accession: S60614		A;Accession: S60614
		A;Status: preliminary; nucleic acid sequence not shown		A;Status: preliminary; nucleic acid sequence not shown
		A;Molecule type: mRNA		A;Molecule type: mRNA
		A;Residues: 1-372 <TPN>		A;Residues: 1-372 <TPN>
		A;Cross-references: GB:S54212; NID:9265055; PID:g265056		A;Cross-references: GB:S54212; NID:9265055; PID:g265056
		A;Cross References: GB:S557711; NID:9299331; PID:AAB25290_1; PID:g265056		A;Cross References: GB:S557711; NID:9299331; PID:AAB25290_1; PID:g265056
		A;Experimental source: Sprague-Dawley, brain		A;Experimental source: Sprague-Dawley, brain
		A;Title: Ciliary neurotrophic factor receptor; cytokine receptor homology: immu		A;Title: Ciliary neurotrophic factor receptor; cytokine receptor homology: immu
		A;Reference number: A47387; PMID:8460125		A;Reference number: A47387; PMID:8460125
		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:39-91/Domain: immunoglobulin homology <IMM>		F:39-91/Domain: immunoglobulin homology <IMM>
		A;Reference number: A47387		A;Reference number: A47387
		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:116-296/Domain: cytokine receptor homology <CRS>		F:116-296/Domain: cytokine receptor homology <CRS>
		A;Reference number: A47387		A;Reference number: A47387
		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:116-296/Domain: cytokine receptor homology <CRS>		F:116-296/Domain: cytokine receptor homology <CRS>
		A;Reference number: A47387		A;Reference number: A47387
		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:116-296/Domain: cytokine receptor homology <CRS>		F:116-296/Domain: cytokine receptor homology <CRS>
		A;Reference number: A47387		A;Reference number: A47387
		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:116-296/Domain: cytokine receptor homology <CRS>		F:116-296/Domain: cytokine receptor homology <CRS>
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		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
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		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:116-296/Domain: cytokine receptor homology <CRS>		F:116-296/Domain: cytokine receptor homology <CRS>
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		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:116-296/Domain: cytokine receptor homology <CRS>		F:116-296/Domain: cytokine receptor homology <CRS>
		A;Reference number: A47387		A;Reference number: A47387
		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:116-296/Domain: cytokine receptor homology <CRS>		F:116-296/Domain: cytokine receptor homology <CRS>
		A;Reference number: A47387		A;Reference number: A47387
		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:116-296/Domain: cytokine receptor homology <CRS>		F:116-296/Domain: cytokine receptor homology <CRS>
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		A;Status: preliminary		A;Status: preliminary
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		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:116-296/Domain: cytokine receptor homology <CRS>		F:116-296/Domain: cytokine receptor homology <CRS>
		A;Reference number: A47387		A;Reference number: A47387
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		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:116-296/Domain: cytokine receptor homology <CRS>		F:116-296/Domain: cytokine receptor homology <CRS>
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		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:116-296/Domain: cytokine receptor homology <CRS>		F:116-296/Domain: cytokine receptor homology <CRS>
		A;Reference number: A47387		A;Reference number: A47387
		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
		F:116-296/Domain: cytokine receptor homology <CRS>		F:116-296/Domain: cytokine receptor homology <CRS>
		A;Reference number: A47387		A;Reference number: A47387
		A;Status: preliminary		A;Status: preliminary
		A;Molecule type: mRNA		A;Molecule type: mRNA
		Query Match 17.2%; Score 392; DB 2; Length 372;		A;Residues: 1-260 'D'
		Best Local Similarity 31.9%; Pred. No. 7.9e-19; Matches 113; Conservative 49; Mismatches 164; Gaps 12;		A;Cross-references: Proc. Natl. Acad. Sci. U.S.A. 90: 2222-2226, 1993
		A;Keywords: growth factor receptor		A;Keywords: growth factor receptor
		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen		A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen

F;2-89/Domain: immunoglobulin homology <IMM>
F;114-294/Domain: cytokine receptor homology <CRS>

Query Match	Match	Score	Length	Best Local Similarity	Pred. No.	Length	Best Local Similarity	Score	Length	
Best Local Similarity	16.7%	Score	380;	DB 2;	Length	362;	30.1%	379;	DB 1;	
Matches	119;	Pred. No.	4.8e-18;	Mismatches	53;	Length	362;	Pred. No.	5.7e-18;	
Qy	2	SSCCGGLSRVIVAYATALYASSSPCOPAQMPGVYQGPGRSVKLCCPEVTAQDPVSWEF	61	Indels	56;	Gaps	16;	Mismatches	122;	
Db	7	SACCVYLAAYVYYAQRHSDQS-----HICQYERGADYTMKCGSMWDAAVITWA	57					Conservative	47;	
Qy	62	DGEPKLQLQDPSGL_GHELVLAQADSTDEGTYCQTLDCG---LGTVLQLGGYPARPV	117					Matches	122;	
Db	58	NG----TDIDSHLNGSYLILKNDLTSQGQSC--YESSHWHIKYQYLRLvPPKESV	111					Local	68;	
Qy	118	VSCQADY-ENFSCTWS-PSQISGLPTRLTYSRKKTVLGADSQRSPSTGWPWPCPDPL	175					Similarity	68;	
Db	112	LMCRSNNNPKFGTYCSWHLPS----PTVNPSPNISVHG-----TREVCERDF	157						Gaps	15;
Qy	176	GAACVYHGAEFNS-QYRINTEVNPLGASTRLLDVSQSLRDPDQQGLRVESPVGP	233							
Db	158	PKNCHIRYLQLFETVKVTKYTNALKNSTLTFEFAVKAQDPESSVAKPVNNP	217							
Qy	234	RRLASWTPASWPQCPHFLKFLRQLRPAQHPAWSTVEP-GLEEVITDAVAGLPHAVR	292							
Db	218	RRLYESWNQNPSSNPDPSEFPLKEFLRPLLIDQWQHVLSQTSHTTDAVAGKEYLQ	277							
Qy	293	V SARDFLDAGTWSTWSPEAWGTPSTGTIPKEI PAWGOLHTEPEVQYDSPA PAPRPSLQP	352							
Db	278	VAAKD-NDIGTWSDWAVHAPEWTE-PKHLTT--EVQITETTSTSTSSPP-----P	328							
Qy	353	HPRLLDHRSVQEVA-----VLA SLGIL 375								
Db	329	TTKICDKGVGSAGAVAYCWTLAYGVLAAYGV 360								

RESULT 7

UHIIUCN

ciliary neurotrophic factor receptor alpha precursor - human

N;Alternate names: CNTR receptor

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999

C;Accession: A40854; A56526

R;Davis, S.; Aldrich, T.H.; Valenzuela, D.M.; Wong, V.; Furth, M.B.; Squinto, S.P.; Yanc

Science 253, 59-63, 1995

A;Title: The receptor for ciliary neurotrophic factor

A;Reference number: A40854; MUID:91289158; PMID:1648265

A;Accession: A40854

A;Molecule type: mRNA

A;Residues: 1-372 <DAV>

A;Cross-references: GB:M73238

R;Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Brannan, C.I.; McClain,

Genomics 15, 157-163, 1995

A;Title: Genomic organization and chromosomal localization of the human and mouse genes

A;Reference number: A56526; MUID:95293367; PMID:7774913

A;Molecule type: DNA

A;Residues: 1-346, 'S', 348-372 <VAL>

A;Cross-references: GB:L38025; NID:960854; PID:9608656

C;Comment: The CNTR receptor is attached to the membrane by a glycosylphosphatidylinositol

C;Comment: The CNTR receptor sequence appears to contain several PEST regions.

C;Genetics:

A;Gene: GDI:CNTR

A;Cross-references: GDB:134652; OMIM:118946

A;Map position: 9p13-9p13

C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog

C;Keywords: glycoprotein; growth factor receptor; membrane protein; phosphatidylinositol

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-372/Product: ciliary neurotrophic factor receptor #status predicted <MAT>

F;39-91/Domain: immunoglobulin homology <IMM>

F;46-89/Disulfide bonds: #status predicted <CRS>

F;60,70,142,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

RESULT 8

A41242

interleukin-6 receptor precursor - human

N;Contains: interleukin-6 receptor, soluble form

C;Species: Homo sapiens (man)

C;Date: 27-Mar-1992 #sequence 02-Dec-1994 #text_change 21-Jul-2000

C;Accession: A41242; JU0080; S17468; A61459; S14621

R;Yamasaki, K.; Taga, T.; Hirata, Y.; Kawanishi, Y.; Seed, B.; Taniguchi,

Science 241, 825-828, 1988

A;Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor

A;Reference number: A41242; MUID:88305347; PMID:316546

A;Accession: A41242

A;Molecule type: mRNA

A;Residues: 1-448 <RN>

A;Cross-references: GB:M0566; PID:CAA31312.1; PID:933846

R;Yamasaki, K.; Taga, T.; Hirata, Y.; Kawanishi, Y.; Seed, B.; Taniguchi,

Proc. Jpn. Acad. 64, 209-211, 1988

A;Title: Molecular structure of interleukin 6 receptor.

A;Reference number: JU0080

A;Molecule type: mRNA

A;Residues: 1-168 <DA2>

R;Schooltink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinr

Biochem. J. 277, 659-664, 1991

A;Title: Structural and functional studies on the human hepatic interleukin-6 receptor.

A;Reference number: S17468; MUID:901336983; PMID:1872801

A;Accession: S17468

A;Molecule type: mRNA

A;Residues: 1-468 <RN>

A;Experimental source: hepatoma cell line HepG2

R;Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M.

J. Exp. Med. 170, 1409-1414, 1989

A;Title: Soluble cytokine receptors are present in normal human urine.

A;Reference number: A61459; MUID:3529343

A;Accession: A61459

A;Molecule type: protein

A;Residues: 20-49 <NOV>

C;Comment: Through this receptor, interleukin-6 induces proliferation, activation, an

C; Comment: This growth factor receptor does not have a tyrosine kinase domain.

C; GeneLoci: ;

A; Gene: GRB:IL6R

A; Cross-references: GDB:127966; OMIM:147880

A; Map position: 1q21-1q21

C; Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog

C; Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein

F; 1-19/Domain: signal peptide; cytokine receptor #status predicted <SIG>

F; 20-468/Domain: interleukin 6 receptor #status predicted <MAT>

F; 20-363/Domain: extracellular #status predicted <EXT>

F; 40-98/Domain: immunoglobulin homology <IMM>

F; 121-309/Domain: cytokine receptor homology <CRS>

F; 364-386/Domain: transmembrane #status predicted <TM>

F; 387-468/Domain: intracellular #status predicted <INT>

F; 47-96/Disulfide bonds: #status predicted

F; 55, 93, 221, 245, 350/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.8%; Score 360; DB 1; Length 468;

Best Local Similarity 28.4%; Pred. No. 1.3e-16; Indels 57; Gaps 19;

Matches 129; Conservative 57; Mismatches 196; Indels 72; Gaps 19;

Query 1 MSSSCGSLSRVLYAVATALYSASSPCPQAWGPPGVQYGPGRSVKLCCPGVTAGD-pvS 58

Db 2 LAVGALLAALLAAFAAAL-APPRCAQAFQVARSQVLTSPGDSTVLTCVEPEPDNATVH 59

Query 59 WFRDGEPKLQQGPD-----SGLGHEHLVLAQADSTDEGTYICQTLGAGGTVTQLQI 110

Db 60 W-----VLRKPAAGSHPSRWAGMGRRLLRLRSVQLHDSDGNNSCYRA-GRPAGTVHLVD 111

Query 111 YPPARPVVSC-QAADYENFSTCWWSPOISQISGLPTRYLSYRKRTVYLGADSQRSPSTG-pw 168

Db 112 VPPEBPQLSFRKSPLSNVCEWGPRTSPSLTT-----KAVLVRKQFNSPAEDFOE 163

Query 169 PC----PQDFIGAACRVVIGAEEFSQYRNTEYNPLGAS-TRLLDVSSQSLIRLPDPPG 223

Db 164 PQYQSQESQRFSCQALAVPDS--SFYIVSMCVYASSGSFSKQTFCQGCLQDPANN 221

Query 224 LRVESPGYPRRLRASWTYPASWCOPHYLLKFLQYRPQAQHPWSTVPGALLE-vIT 281

Db 222 ITVTAVARNPRWLSTVWQDHSWN-SSEFYRLFELRYRAERSKTFTTNWVKDLOHHCVTH 280

Query 282 DAVAGLPHAVRVSARDFLDAGTWSTWSPWAHGTTSTGTLPKEPAWQQLHQTPEVEPOVD 341

Db 281 DAWSSLURHVQLRAQEFGGEWSEWSPEAMGTWTES-----RSPPAENEVS 328

Query 342 SPAPPRLPSLQPHPRILLDHRSSQEVY---LASIGLISFLGVLVAGALP----- 388

Db 329 TPMQALTINDDDNIL-FRISANATSLSLVPDSSVYPLPTFL-VAGGSIAFTLILCIAIVL 386

Query 389 ----LW-LRLRRGGKDKGSPKPGFELASVIVPDRP 417

Db 387 RFKKTKWKLRAKEGRTSMHPPYSLGQLVPERPRP 420

Query Match 13.1%; Score 298.5; DB 1; Length 462;

Best Local Similarity 27.2%; Pred. No. 1.6e-12; Indels 1.23; Gaps 25;

Matches 132; Conservative 50; Mismatches 181; Indels 1.23; Gaps

Query 1 MSSSCGSLSRVLYAVATALYSASSPCPQAWGPPGVQYGPGRSVKLCCPGVTAGD-pvS 58

Db 2 LAVGALLAALLAAFAAAL-APPRCAQAFQVARSQVLTSPGDSTVLTCVEPEPDNATVH 59

Query 59 WFRDGEPKLQQGPD-----SGLGHEHLVLAQADSTDEGTYICQTLGAGGTVTQLQI 110

Db 60 W-----VLRKPAAGSHPSRWAGMGRRLLRLRSVQLHDSDGNNSCYRA-GRPAGTVHLVD 111

Query 111 YPPARPVVSC-QAADYENFSTCWWSPOISQISGLPTRYLSYRKRTVYLGADSQRSPSTG-pw 168

Db 115 LSCFRKKNPLNVAECWHPSSTPS-PTKRAVMFAKKI-----NTNGKSDFQVPQYSQQL 168

Query 176 GAARCVHGAEEFWSOYR-NVTEYNPLGASTRLDVLSOSI-LRPDPPOGLRVEVSPG- 231

Db 169 KSFSCDEVETLEGGDVKYHVSLSLVCANSVG-SRSSINQVCFDLDLYGORFFTV-WPLQ-----VAQHQC 274

Query 268 WSTVPGAGLEEVITDAVGLPHAVRVSARDFLDAGTWSTWSPEAWGTPSTGTIPKEIPAW 327

Db 275 -----VHDALRGYKHVVQVRGKEFDGQWSKWSPEVTGTP-----W 312

Query 328 GQLHTQPEVERQVDSPAAPRPSLQPHPRLLDHRD---SVEQAVLA-----SLGILSF 377

Db 313 ---LAEPRTPAGIPGPNPQTSVSYD-----NHEDQGSSSEATVAPYQGSSPILPPTF 366

Query 378 LGLVAGALAGLW-----LRLRQGKD-----GSPKPGFLASVIVPDR 415

Db 367 L-VAGGSIAFLGLLICVFILRLKKWKWSQAEEKESKTTSPPPYPLGQPLKPTFL--LVPLLT 423

Query 416 RPGAPN 421

Db 424 PSGSHN 429

RESULT 10

150455 prolactin receptor - pigeon

C; Species: Columba livia (domestic pigeon)

C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000

C; Accession: I50455

R; Chen, X.; Horserman, N. D.

Endocrinology 135, 269-276, 1994

A; Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor

A; Reference number: I50455; MUID:3428367; PMID:516866

A; Status: preliminary; translated from GB/EMBL/DBBJ

A; Molecule type: mRNA

A; Residues: 1-830 <CHE>

A; Cross-references: EMBL:U07694; NID:9466381; PID:AAA20646.1; PMID:9466382

A; Superfamily: cytokine receptor homology <CRS1>

F; 240-426/Domain: cytokine receptor homology <CRS2>

Query Match 9.7%; Score 221; DB 2; Length 830;

Best Local Similarity 29.0%; Pred. No. 4e-07; Indels 36; Mismatches 90; Gaps 12;

Matches 67; Conservative 53; Gaps 38; Indels 38; Gaps 12;

Query 111 YPPARPVVSCQADYENFSCWTWSPSQISGLPTRYLTSYRKTKVILGADSQRSPSTGPWPC 170

RESULT 9

A37986 interleukin-6 receptor precursor - rat

N; Alternate names: IL-6 receptor

C; Species: Rattus norvegicus (Norway rat)

C; Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999

C; Accession: A37986

R; Baumann, M.; Baumann, H.; Fey, G. H.

J. Biol. Chem. 265, 19853-19852, 1990

A; Title: Molecular cloning, characterization and functional expression of the rat liver

A; Reference number: A37986; MUID:91060602; PMID:2174054

A; Molecule type: mRNA

A; Residues: 1-462 <BAU>

A; Cross-references: GB:M58587; PID:904921; PID:g204922

C; Comment: After binding IL-6, this chain associates with a 130K glycoprotein that is es

C; Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog

F; 1-19/Domain: signal sequence #status predicted <SIG>

RESULT 11	
Q01655	prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)	
C:Date: 30-Sep-1993 #sequence_revision	30-Sep-1993 #text_change
C:Accession: J01655	28-Jul-2000
C:Author: R.Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.	
C:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence	
A:Reference number: J01655	
A:Accession: J01655	
A:Molecule type: mRNA	
A:Residues: 1-831 <TAN>	
A:Cross references: DBJ:D13154; NID:9222848; PIDN:BR02439.1; PMID:9222849	
A:Experimental source: kidney	
C:Superfamily: cytokine receptor homology	
C:Keywords: glycoprotein; transmembrane protein	
C:1-23/Domain: signal sequence #status predicted <SIG>	
C:23-36-219/Domain: prolactin receptor #status predicted <MAT>	
C:239-425/Domain: cytokine receptor homology <CRS1>	
C:7-24/Domain: cytokine receptor homology <CRS2>	
C:59-91/Domain: transmembrane domain: predicted <TM>	
C:59-91/100-112/Domain: transmembrane domain: predicted <TM>	
C:101-900/Domain: transmembrane domain: predicted <TM>	

A;Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin receptors in bovine tissues
A;Reference number: I45971; MUID:93246019; PMID:1338725
A;Accession: I45971
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-501 <SCOP>
A;Cross-references: GB:L02549; NID:9163617; PID:AAA51417.1; PMID:9163618
C;Genetics:
C;Superfamily: cytokine receptor homology_F:36-221/Domain: cytokine receptor homology <CRS>
Query Match Score 9.0%; Length 581;
Best Local Similarity 26.5%; Pred. No. 3.4e-06;
Matches 61; Conservative 36; Mismatches 92; Indels 41; Gaps 11;
Qy 112 PPARP-VVSCQAADEFNFSCTWSPS0ISGLPTRYLTSYRKTKTVLGADSQRSSPSTGPWPC 170
Db 27 PPEKPLVKCRSPGKETFTCWEPGADGGLPTNYTKHE-----GETLIHEC 75
Qy 171 PQDPLGAARCVVHGG --AEFNSQYRINTVEVNPLG ASTRELVDLSQSLRDPDPPQGLRV 226
Db 76 PDYKTGGPNCSCYFSKKHTSIWKMYVITVNA INQMGISSSDPLVYHVTYIVEPEPPNLTL 135
Qy 227 ESVPSYPRR -LRAWSWTP-----ASWPQCOPHFLIKFRFLQYRPAQHPAWS--TVEPAG 275
Db 136 ELKHPEDRKEYLWKWSPPTMDVKSgw----FIQYERLRLKPERATDWEHTFLKQTQ 190
Qy 276 LEEVITDAAGLPHAVRSARDFELDAGTWSTWSPEAWGTPSTGTPEKEIP 325
Db 191 LK - IFNLYPGQKTVLQIRCKP -DHGYNSEWSP-----SSIQ1PNDFP 231

RESULT 13

A30304
prolactin receptor 2 precursor - rabbit
N;Alternate names: prolactin receptor, mammary gland
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Jul-2000
C;Accession: A30304; A60380
R;Elder, M.; Jolicoeur, C.; Levi-Meyrueis, C.; Dusantier-Fourt, I.; Petridou, B.; Bout
Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
A;Title: Identification and sequence analysis of a second form of prolactin receptor
A;Reference number: A30304; MUID:99184578; PMID:22898321
A;Accession: A30304
A;Molecule type: mRNA
A;Residues: 1-616 <EDE>
A;Cross references: GB:J04510; NID:9165669; PIDN:AAA31457.1; PMID:9165670
R;Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
Int. J. Biochem. 22, 1089-1095, 1990
A;Title: Purification and partial sequence of the rabbit mammary gland prolactin receptor
A;Reference number: A30304; MUID:91146782; PMID:2289615
A;Accession: A60380
A;Molecule type: protein
A;Residues: 41-58, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108;150-164, 'XX',
A;Note: the amino end of the mature protein was blocked
C;Superfamily: cytokine receptor homology
C;Keywords: blocked amino end; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-67/Domain: prolactin receptor homology <CRS>
F:36-221/Domain: cytokine receptor homology <CRS>

RESULT 12
45971
prolactin receptor - bovine
Species: Bos primigenius taurus (cattle)
Date: 16-Aug-1996 #sequence_revision 16-Aug-1996
Accession #: I45971
Scott, P.; Kessler, M.A.; Schuler, L.A.
text_change 28-Jul-2000

Db 76 PDYKTPGPNSCYFSKKHTSLWVYIYTIVNATNQGSSVSDPRTVDVTY--TVEPDPPVNL 133
 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Mar-2002
 C;Accession: A59405; A49400
 R;Hu, Z.Z.; Meng, J.; Dufau, M.L.
 J. Biol. Chem. 276, 41086-41094, 2001
 A;Title: Isolation and characterization of two novel forms of the human prolactin receptor gene: A59405; MUID:21538812; PMID:11518703
 A;Accession: A59405
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-376 <HUL>
 R;Hu, Z.Z.
 submitted to GenBank, December, 1999
 A;Reference number: A49400
 A;Accession: A49400
 A;Cross-references: GB:AF214012; PIDN:AF214012.1
 R;Hu, Z.Z.
 A;Species: Homo sapiens (man)
 C;Accession: B59405; B49400
 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Mar-2002
 R;Hu, Z.Z.; Meng, J.; Dufau, M.L.
 J. Biol. Chem. 276, 41086-41094, 2001
 A;Title: Isolation and characterization of two novel forms of the human prolactin receptor gene: A59405; MUID:21538812; PMID:11518703
 A;Accession: B59405
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: GB:AF214012; PIDN:AF214012.1
 R;Hu, Z.Z.
 A;Cross-references: GB:AF214012; PIDN:AF214012.1
 A;Reference number: A49400
 A;Accession: B49400
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-288 <HUL>
 C;Comment: This is one of the short forms (Sla and Sib) of the human proactin receptor gene. It is less effective than Sla. However, their ligand-binding domain is identical.
 C;Genetics:
 A;Gene: GDB:PRLR
 A;Cross-references: GDB:120315; OMIM:176761
 A;Map position: 5p13.3-p13.1
 C;Superfamily: cytokine receptor homology
 C;Keywords: glycoprotein; transmembrane protein
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-376/Product: prolactin receptor, short form Sla #status predicted <MAT>
 F;36-221/Domain: cytokine receptor homology <CRS>
 F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 8.3%; Score 189; DB 2; Length 376;
 Best Local Similarity 28.2%; Pred. No. 2.2e-05;
 Matches 60; Conservative 27; Mismatches 92; Indels 34; Gaps 10;
 Db 27 PPGKPEIFCRSPNKEFTCWWRPTDGGIPTNVLTY-----HREGETLMHEC 75
 Qy 171 PQDPLGAARCVHGAEF--WSQYRINTTEVNPLGAS-TRLIDVSLSQSTLRRDPDPQQGLRV 226
 C;Comment: This is one of the short forms (Sla and Sib) of the human prolactin receptor gene. It is less effective than Sla. However, their ligand-binding domain is identical.
 C;Genetics:
 A;Gene: GDB:PRLR
 A;Cross-references: GDB:120315; OMIM:176761
 A;Map position: 5p13.3-p13.1
 C;Superfamily: cytokine receptor homology
 C;Keywords: glycoprotein; transmembrane protein
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-288/Product: prolactin receptor, short form Sib #status predicted <MAT>
 F;36-221/Domain: cytokine receptor homology <CRS>
 F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
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 Best Local Similarity 28.2%; Pred. No. 1.7e-05;
 Matches 60; Conservative 27; Mismatches 92; Indels 34; Gaps 10;
 Db 136 EVKQPEDRKPKYLWIKWSPPTFLIDLKTVW-----FTLYEIRLKPEKAEME-IHFAGQQT 189
 Qy 277 EEVITDAVGLPHAVRVSARDFLDAGTWSTWSP 309
 C;Comment: This is one of the short forms (Sla and Sib) of the human prolactin receptor gene. It is less effective than Sla. However, their ligand-binding domain is identical.
 C;Genetics:
 A;Gene: GDB:PRLR
 A;Cross-references: GDB:120315; OMIM:176761
 A;Map position: 5p13.3-p13.1
 C;Superfamily: cytokine receptor homology
 C;Keywords: glycoprotein; transmembrane protein
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-376/Product: prolactin receptor, short form Sib #status predicted <MAT>
 F;36-221/Domain: cytokine receptor homology <CRS>
 F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 8.3%; Score 189; DB 2; Length 376;
 Best Local Similarity 28.2%; Pred. No. 2.2e-05;
 Matches 60; Conservative 27; Mismatches 92; Indels 34; Gaps 10;
 Db 190 EFKILSLHFGQKYLVQVRCKP--DHGYNSAWSP 220
 Qy 227 ESYVGYPRR--LRASTWTP-----ASWPCQPHFLKERQYRPAOHPAWSTVEPAG--L 276
 C;Comment: This is one of the short forms (Sla and Sib) of the human prolactin receptor gene. It is less effective than Sla. However, their ligand-binding domain is identical.
 C;Genetics:
 A;Gene: GDB:PRLR
 A;Cross-references: GDB:120315; OMIM:176761
 A;Map position: 5p13.3-p13.1
 C;Superfamily: cytokine receptor homology
 C;Keywords: glycoprotein; transmembrane protein
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-376/Product: prolactin receptor, short form Sib #status predicted <MAT>
 F;36-221/Domain: cytokine receptor homology <CRS>
 F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 8.3%; Score 189; DB 2; Length 376;
 Best Local Similarity 28.2%; Pred. No. 2.2e-05;
 Matches 60; Conservative 27; Mismatches 92; Indels 34; Gaps 10;
 Db 190 EFKILSLHFGQKYLVQVRCKP--DHGYNSAWSP 220
 Qy 277 EEVITDAVGLPHAVRVSARDFLDAGTWSTWSP 309
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 C;Genetics:
 A;Gene: GDB:PRLR
 A;Cross-references: GDB:120315; OMIM:176761
 A;Map position: 5p13.3-p13.1
 C;Superfamily: cytokine receptor homology
 C;Keywords: glycoprotein; transmembrane protein
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-376/Product: prolactin receptor, short form Sib #status predicted <MAT>
 F;36-221/Domain: cytokine receptor homology <CRS>
 F;59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 8.3%; Score 189; DB 2; Length 376;
 Best Local Similarity 28.2%; Pred. No. 2.2e-05;
 Matches 60; Conservative 27; Mismatches 92; Indels 34; Gaps 10;
 Db 190 EFKILSLHFGQKYLVQVRCKP--DHGYNSAWSP 220

RESULT 15
 A59405
 prolactin receptor short form Sla precursor, breast cancer cells T-47D - human
 C;Species: Homo sapiens

Search completed: January 17, 2003, 19:39:58
 Job time : 26 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:38:14 ; Search time 13 Seconds
 (without alignments)
 645.0287 Million cell updates/sec

Title: US-09-924-338-2
 Perfect score: 2275
 Sequence: 1 MSSSSGGLSRVLYAVATALV KPGFLASVIPYDRRGAPNL 422

Scoring table: BLOSUM62
 Gapop 10.0 , Capext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA : *
 1: /cgn2_6/pctodata/1/pubpaa/us08_NEW_PUB.pep: *
 2: /cgn2_6/pctodata/1/pubpaa/PCT_NEW_PUB.pep: *
 3: /cgn2_6/pctodata/1/pubpaa/us06_NEW_PUB.pep: *
 4: /cgn2_6/pctodata/1/pubpaa/us06_PUBCOMB.pep: *
 5: /cgn2_6/pctodata/1/pubpaa/us07_PUBCOMB.pep: *
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 8: /cgn2_6/pctodata/1/pubpaa/us08_PUBCOMB.pep: *
 9: /cgn2_6/pctodata/1/pubpaa/us09_NEW_PUB.pep: *
 10: /cgn2_6/pctodata/1/pubpaa/us09_PUBCOMB.pep: *
 11: /cgn2_6/pctodata/1/pubpaa/us11_NEW_PUB.pep: *
 12: /cgn2_6/pctodata/1/pubpaa/us10_PUBCOMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2275	100.0	422	10 US-09-924-338-2	Sequence 2, Appli
2	1831	80.5	441	10 US-09-924-338-4	Sequence 4, Appli
3	339	14.9	1158	9 US-09-935-868-24	Sequence 26, Appli
4	332	14.6	1168	9 US-09-935-868-24	Sequence 24, Appli
5	329.5	14.5	360	9 US-09-935-868-15	Sequence 15, Appli
6	329.5	14.5	592	9 US-09-935-868-8	Sequence 8, Appli
7	313	13.8	315	9 US-09-935-868-16	Sequence 16, Appli
8	255.5	11.2	229	9 US-10-000-776-10	Sequence 10, Appli
9	255.5	11.2	229	9 US-09-911-497-12	Sequence 12, Appli
10	212.5	9.3	389	10 US-09-880-578-27	Sequence 27, Appli
11	211.5	9.3	389	10 US-09-880-578-24	Sequence 24, Appli
12	211.5	9.3	389	10 US-09-880-578-29	Sequence 29, Appli
13	211.5	9.3	421	9 US-09-037-657-44	Sequence 44, Appli
14	211.5	9.3	422	9 US-09-944-413-32	Sequence 32, Appli
15	211.5	9.3	422	9 US-09-944-403-32	Sequence 32, Appli
16	211.5	9.3	422	9 US-09-944-896-32	Sequence 32, Appli
17	211.5	9.3	422	9 US-09-944-944-32	Sequence 32, Appli
18	211.5	9.3	422	9 US-09-944-907-32	Sequence 32, Appli
19	211.5	9.3	422	9 US-09-944-929-32	Sequence 32, Appli

ALIGNMENTS

RESULT 1 US-09-924-338-2	Sequence 2, Application US/09924338 Patent No. US200208223A1	GENERAL INFORMATION: APPLICANT: Tobin, James TITLE OF INVENTION: HUMAN INTERLUEKIN-11 RECEPTOR NUMBER OF SEQUENCES: 4	CORRESPONDENCE ADDRESS: ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive CITY: Cambridge STATE: MA COUNTRY: USA ZIP: 02140	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, version #1.25
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CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/924, 338	FILING DATE: 07-Aug-2001	CLASSIFICATION: <Unknown>	PRIOR APPLICATION NUMBER: 09/151,102	FILING DATE: 1998-09-00
ATTORNEY/AGENT INFORMATION: NAME: Brown, Scott A. REGISTRATION NUMBER: 32,724	APPLICATION NUMBER: 09/362, 304	TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8224	TELEFAX: (617) 876-5831	SEQUENCE CHARACTERISTICS: LENGTH: 422 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 100.0%; Score 2275; DB 10; Length 422;

Best Local Similarity 100.0%; Pred. No. 5e-144;

Matches 422; Conservative 0; Mismatches 0; Gaps 0;

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Db 1 MSSCCSGLSRVIVAVATLYSASSCPQAMPGPYQGPGRSYKVLCCPBTAGDPVSWF 60

Qy 61 RDGEKPLLQGPDGLGHELVLAQADSTDETRTYSRKTKTVLGADSORSPSTGPHNCPQDPLGAARC 120

Db 61 RDGEKPLLQGPDGLGHELVLAQADSTDETRTYSRKTKTVLGADSORSPSTGPHNCPQDPLGAARC 120

Qy 121 QAADYENFSCTWPSQTSQISLQPTTRVLTYSRKTKTVLGADSORSPSTGPHNCPQDPLGAARC 180

Db 121 QAADYENFSCTWPSQISLQPTTRVLTYSRKTKTVLGADSORSPSTGPHNCPQDPLGAARC 180

Qy 181 VVHGAEEFWSOYRINTVEVNLCASTRLDVSLSQSLRDPDQGJURVESPGYPRRLRASW 240

Db 181 VVHGAEEFWSOYRINTVEVNLCASTRLDVSLSQSLRDPDQGJURVESPGYPRRLRASW 240

Qy 241 TYPASWPCCOPHFLLKFRLOYRPAOHAWSTVEPAGLEEVITDAVAGLPHAVRYSARDFLD 300

Db 241 TYPASWPCCOPHFLLKFRLOYRPAOHAWSTVEPAGLEEVITDAVAGLPHAVRYSARDFLD 300

Qy 301 AGTWSTWSPEAWGTPSTGTIPKEIPAWGQLHTQPEVEQVDSAPPRPSLQHPPLLDHR 360

Db 301 AGTWSTWSPEAWGTPSTGTIPKEIPAWGQLHTQPEVEQVDSAPPRPSLQHPPLLDHR 360

Qy 361 DSVEQVAVLASIGLTSFLGLVAGALGILWLRGGDKGSKPGEFLASVIVPDRRGASP 420

Db 361 DSVEQVAVLASIGLTSFLGLVAGALGILWLRGGDKGSKPGEFLASVIVPDRRGASP 420

Qy 421 NL 422

Db 421 NL 422

RESULT 2

US-09-924-338-4

; Sequence 4, Application US/09924338

; Patent No. US20020083233A1

; GENERAL INFORMATION:

; APPLICANT: Tobin, James

; TITLE OF INVENTION: HUMAN INTERLEUKIN-11 RECEPTOR

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 Cambridgepark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/924,338

; FILING DATE: 07-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/151,102

; FILING DATE: 1998-09-10

; APPLICATION NUMBER: 08/362,304

; FILING DATE: 22-DEC-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Brown, Scott A.

; REGISTRATION NUMBER: 32,724

; REFERENCE/DOCKET NUMBER: G15252

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8224

; TELEFAX: (617) 876-5651

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 441 amino acids

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

; US-09-924-338-4

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2; Gaps 1;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; Gaps 1;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Gaps 1;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; Gaps 1;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Gaps 1;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; Gaps 1;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Gaps 1;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; Gaps 1;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Gaps 1;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; Gaps 1;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Gaps 1;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; Gaps 1;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Gaps 1;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; Gaps 1;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Gaps 1;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; Gaps 1;

; SEQ ID NO: 4:

RESULT 4
US-09-935-868-24
; Sequence 24, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc.
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIORITY FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-868-15

Query Match 14.5%; Score 329.5; DB 9; Length 360;
Best Local Similarity 29.2%; Pred. No. 4; 8e-15; Indels 53; Gaps 15;
Matches 112; Conservative 46; Mismatches 172; Delins 1; Gaps 1;

Qy 5 CGSLRSRVLVAVATALYSASSPCPOAWGPPQYQGPGRSYKLCCPGVTAQD--PVSFRD 62
Db 6 CALLAALLAAPGAAL--APRCPAQAVARGVLTSGDSTVLTCPEVEPEDNATVHW--- 60

Qy 63 GEPKLLQGPD-----SGIGHELVLAQADSTDECTYICOTLDGALGGPVTLQGYPPA 114
Db 61 ---VLRKPAAAGSHPSRWAQMGRILLRSVQLHDHCVTHDANS 284

Qy 115 RPVVSQ-QAADDENFQCTWPSQISQPLTYLTSRKKTVLGADSQRSPSTG-PWPC-- 170
Db 116 EPQLSFRKSPLSNVYCEWGRSTSLTT-----KAVLLVRKFQNSAEDFREPCQY 167

Qy 171 --PQDPLGAACRVVHGAEFNSQYRFNTEVNPGLAS-TRILDVSLQSILRPDPDPPANITYV 227

Qy 168 SQESQFSCQLAQPEDS--SFYIVSMCVAASSVGSKFSKQTFOGGILQDPDPPANITYV 225

Qy 228 SVPGYPRRLRASWTPSWSQPHFLKFLRIQYRAQHPAWSVTPAGEE--VITDAVA 285
Db 226 AVARNPWLSTWQDHSHWN-SSFYRLRERYRAERSKTTWAKDLOHHCVTHDANS 284

Qy 286 GLPHAVRVSARDFLDAGTWTWSPEAWGTPSTGTIPKEIPIAWGQHTQPEVEPVQDSDPA 345
Db 285 GLRHVVQLRAQEFGGEWSEWSPEAMGTWTES--RSPPAENEVSTPMELDPCGYISP 342

Qy 346 PRPSLQPH 353
Db 343 ESPVWQLH 350

RESULT 4
US-09-935-868-24
; Sequence 24, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc.
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIORITY FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 24
; LENGTH: 1168
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-868-24

Query Match 14.4%; Score 332; DB 9; Length 1168;
Best Local Similarity 30.2%; Pred. No. 1.2e-14; Indels 60; Gaps 16;
Matches 114; Conservative 42; Mismatches 161; Delins 1; Gaps 1;

Qy 5 CGSLRSRVLVAVATALYSASSPCPOAWGPPQYQGPGRSYKLCCPGVTAQD--PVSFRD 62
Db 6 CALLAALLAAPGAAL--APRCPAQAVARGVLTSGDSTVLTCPEVEPEDNATVHW--- 60

Qy 63 GEPKLLQGPD-----SGIGHELVLAQADSTDECTYICOTLDGALGGPVTLQGYPPA 114
Db 61 ---VLRKPAAAGSHPSRWAQMGRILLRSVQLHDHCVTHDANS 284

Qy 115 RPVVSQ-QAADDENFQCTWPSQISQPLTYLTSRKKTVLGADSQRSPSTG-PWPC-- 170
Db 116 EPQLSFRKSPLSNVYCEWGRSTSLTT-----KAVLLVRKFQNSAEDFREPCQY 167

Qy 171 --PQDPLGAACRVVHGAEFNSQYRFNTEVNPGLAS-TRILDVSLQSILRPDPDPPANITYV 227

Qy 168 SQESQFSCQLAQPEDS--SFYIVSMCVAASSVGSKFSKQTFOGGILQDPDPPANITYV 225

Qy 228 SVPGYPRRLRASWTPSWSQPHFLKFLRIQYRAQHPAWSVTPAGEE--VITDAVA 285
Db 226 AVARNPWLSTWQDHSHWN-SSFYRLRERYRAERSKTTWAKDLOHHCVTHDANS 284

Qy 286 GLPHAVRVSARDFLDAGTWTWSPEAWGTPSTGTIPKEIPIAWGQHTQPEVEPVQDSDPA 345
Db 285 GLRHVVQLRAQEFGGEWSEWSPEAMGTWTES--RSPPAENEVSTPMQ 332

Qy 346 PRPSLQPHPRLDHRDSVEQAV 368
Db 333 ALTTNWDDDNIL-FRDSANATSL 354

RESULT 6
US-09-935-868-8
; Sequence 8, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc.
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935, 868
; PRIORITY FILING DATE: 2002-04-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8

LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-8

Query Match 14.5%; Score 329.5; DB 9; Length 592;
Best Local Similarity 29.2%; Pred. No. 8 4e-15;
Matches 112; Conservative 46; Mismatches 172; Indels 53; Gaps 15;

QY 5 CSGLSRVLVAVATALVASSPCPQAAGPGVQYQGPGRSYVKLCCPGVTAGD--PVSMFRD 62
Db 6 CALLAALAAPGAAL-APRCPAQEVARGVLTSLPGDSVTLCPGVPEPDNATVHW-- 60

QY 63 GEPKLLQGPD-----SGLGHLVLAQADSDTEGYTCQTLGALGGTVTQLQGYPPA 114
Db 61 ----VLRKPAAGSHPSRAGMGRLLRSVOLHDSGNNSCYRA-GRPAGTVLVDVPP 115

QY 115 RPVYSC-QAADDYENFSCTWSPSQTSGLPLTRYLTSYRKTKVLGADSQRSSPSTG-PWPC-- 170
Db 116 EPQLSCFRKSPLSNVCEMGPRSTPLTT-----KAVLVLVRKFQNSPAEDFQEPCQY 167

QY 171 -PQDPGLGARCVHGA-EFWSQYRINTVEVNPGAS-TRLIYSLQSITLRPPOGLRVE 227
Db 168 SQESQFKSCOLAVEPEGDS--SFIVTMSMCVASSYGSKEFKTQTEQGCGILQDPPEANITV 225

QY 228 SVPGYPRRLRASWTYPSAWPCQPHFLKFRQLYRPAQHPAWSITIVEPAGEEE-VITDVA 285
Db 226 AVARNPRNLNSVTWDPHSKW-SSYRLRFELRRAERSKTFITWMVKDLQHICVIHAW 284

QY 286 GLPHAVRVSARDFLDAGTWSTWSPEAWGTPSTGTIPKEIPANGQQLHTOPEVFQVDSAP 345
Db 285 GLRHVVQLEAQQEFGQEMSEWSPEANGTPWTE-----RSPPAENEVSTPMQ 332

QY 346 PRPSLQPHPRLDIIDSVEQVAV 368
Db 333 ALTNKDDDNL-FRDSANATSL 354

RESULT 7
US-09-935-868-16
; Sequence 16, Application US/09935868
; Patent No. US2002-0164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc.
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 16
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-16

Query Match 13.8%; Score 315; DB 9; Length 315;
Best Local Similarity 31.0%; Pred. No. 3.8e-14;
Matches 102; Conservative 38; Mismatches 149; Indels 40; Gaps 13;

QY 5 CSGLSRVLVAVATALVASSPCPQAAGPGVQYQGPGRSYVKLCCPGVTAGD--PVSMFRD 62
Db 6 CALLAALAAPGAAL-APRCPAQEVARGVLTSLPGDSVTLCPGVPEPDNATVHW-- 60

QY 63 GEPKLLQGPD-----SGLGHLVLAQADSDTEGYTCQTLGALGGTVTQLQGYPPA 114
Db 61 ----VLRKPAAGSHPSRAGMGRLLRSVOLHDSGNNSCYRA-GRPAGTVLVDVPP 115

QY 115 RPVYSC-QAADDYENFSCTWSPSQTSGLPLTRYLTSYRKTKVLGADSQRSSPSTG-PWPC-- 170
Db 116 EPQLSCFRKSPLSNVCEMGPRSTPLTT-----KAVLVLVRKFQNSPAEDFQEPCQY 167

QY 171 -PQDPGLGARCVHGA-EFWSQYRINTVEVNPGAS-TRLIYSLQSITLRPPOGLRVE 227
Db 168 SQESQFKSCOLAVEPEGDS--SFIVTMSMCVASSYGSKEFKTQTEQGCGILQDPPEANITV 225

QY 228 SVPGYPRRLRASWTYPSAWPCQPHFLKFRQLYRPAQHPAWSITIVEPAGEEE-VITDVA 285
Db 226 AVARNPRNLNSVTWDPHSKW-SSYRLRFELRRAERSKTFITWMVKDLQHICVIHAW 284

QY 286 GLPHAVRVSARDFLDAGTWSTWSPEAWGTPSTGTIPKEIPANGQQLHTOPEVFQVDSAP 345
Db 285 GLRHVVQLEAQQEFGQEMSEWSPEANGTPWTE-----RSPPAENEVSTPMQ 332

QY 346 PRPSLQPHPRLDIIDSVEQVAV 368
Db 333 ALTNKDDDNL-FRDSANATSL 354

RESULT 8
US-10-000-776-10
; Sequence 10, Application US/10000776
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Pfanz, Stefan K.-H.
; APPLICANT: Kastlein, Robert A.
; APPLICANT: Basan, Jose P.
; APPLICANT: Renick, Dona.
; APPLICANT: de Waal Maleyt, Rene
; APPLICANT: Cheung, Jeanne
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX01040K3
; CURRENT APPLICATION NUMBER: US/10/000,776
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/791,497
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/627,897
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,581
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/147,763
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 10
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-776-10

Query Match 11.2%; Score 255.5; DB 9; Length 229;
Best Local Similarity 30.9%; Pred. No. 2.4e-10;
Matches 73; Conservative 35; Mismatches 95; Indels 33; Gaps 10;

QY 94 CQTLDGAGCAGTVTQLGYPPAR--PVVSCQAAADYE-NFSCWTMS--PQISGLGPTRVTS 147
Db 15 CPCSGRGK-----PPAALTLPQCRCASRYPIAVDCSMTLPPAPNSTSPTSPVFAIT 65

QY 148 YRKKTVLGADSQRSPSTGPQDPGLGAARCVGVBAGEFWSQ--YRINVTEVNPLGAST 205
Db 66 YR---LGMAARGHS---WPLCLQTPTSTSCSTTDYOLFMSMAPYVILNTAVHPWGSS 116

QY 206 RLIDVLSILRDPDQSLRVEVSPGYPRLRASWTYPASWPCQPHFLKFRQLYRPAQH 265
Db 117 SFVPFITHEIIKPDPPGEVRLS--PLARHRVQWEPGSMWPPEIFSKWTRYKROGA 174

QY 266 PMSTVERGLEEVITDAGTWTWSPAWGTGSTG 318
Db 175 ARFHVGPIEATSFILRAVR--BRARYVQVAQDLTUYGELSDWSLJDATMSLG 228

RESULT 9
US-09-791-497-12
; Sequence 12, Application US/09/791497
; Publication No. US20030003343A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.

APPLICANT: Kastelein, Robert A.
 APPLICANT: Bazan, J. Fernando
 APPLICANT: Pflanz, Stefan
 TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
 FILE REFERENCE: DX0104OK2
 CURRENT APPLICATION NUMBER: US/09/791,497
 CURRENT FILING DATE: 2001-02-22
 PRIOR APPLICATION NUMBER: 09/627,897
 PRIOR FILING DATE: 2000-07-27
 PRIOR APPLICATION NUMBER: 60/146,581
 PRIOR FILING DATE: 1999-07-30
 PRIOR APPLICATION NUMBER: 60/147,763
 PRIOR FILING DATE: 1999-08-06
 NUMBER OF SEQ ID NOS: 14
 SEQ ID NO: 12
 LENGTH: 229
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-791-497-12

Query Match 11.28; Score 255.5; DB 9; Length 229;
 Best Local Similarity 30.98; Pred. No. 2.4e-10;
 Matches 73; Conservative 35; Mismatches 95; Indels 33; Gaps 10;

Qy 94 COTLDGALGGTQLQGYPAR--PVSQSCQADYE-NFSCTWS--PSQISGLPTRYTS 147
 Db 15 CPPCSGRKG -----PAATLTLRVQCRASRYPLAVDCSWTLPAPNISTSPIFAT 65

Qy 148 YRKKTIVLGDSQRSPRSPTGPWPCPDPGLGAACRVCVHAEFWSQ--YRINTYEVNPLGAST 205
 Db 66 YR---LGMAARGHS---WCLQOPTPTSTC1TDQFLSMAPVLNNTAVHPWGSSS 116

Qy 206 RLLDVSQSLRDPDPOGLRVESSVPGYPRLRASTWTPASHPCQPHFLKFLRQLYRPAQH 265
 Db 117 SFVPFITEHIKPDPPGVRLS--PLAERHQVQNEPPGSPPEPEFLSFLXWIRYKRQGA 174

Qy 266 PAWSTVEPAGELEEVITDAVAGLPHA--VRVYSAARDFLDAGMWSTSWPEANWTPSTG 318
 Db 175 ARFHRYGPIEATSFILRAVR--PRARYYYQVAQDLTDYGEISDNWLSPATATMSLG 228

RESULT 10
 US-09-880-578-27
 ; sequence 27, Application US/09880578
 ; Patent No. US2002004573A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, Si
 ; Presneil, Scott R.
 ; Gilbert, Anna C.
 ; Foster, Donald C.
 ; Adams, Robyn L.

TITLE OF INVENTION: MAMMALIAN ZCYTORS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: ZymoGenetics
 STREET: 1201 Eastlake Ave East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/880,578
 FILING DATE: 13-Jun-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G.
 REGISTRATION NUMBER: 32,743
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 US-09-880-578-27

Query Match 9.3%; Score 212.5; DB 10; Length 389;
 Best Local Similarity 23.8%; Pred. No. 3e-07;
 Matches 89; Conservative 54; Mismatches 136; Indels 95; Gaps 19;

Qy 17 TALVASSSSPCPAWGPVGQVQGPGRSVKLCC----PGVTAGDPPSWFRIDGE---PKL 67
 Db 3 TAVISQDPTILLI-----GSSLATACSVHSDPPGATA-EGLYWTNLGRRLPPPE 50

Qy 68 LOGPDSGLGHELVLAQAD----STDGEETYCQTLDGALGGTVTOLQGYPPARPV-VSCQ 121
 Db 51 SRVLNAs--TIALALANLNGSRQRSSDNLYCHARDSTILAGSCLVGLPPBKPVNISCW 107

Qy 122 AADYENFSCTNSPSQ--TSGLPTRTRYLSYRKTKVLGADSQRSRSPTGPWPC--PQDPLGA 177
 Db 108 SKRNKDJTCRWPGAIGETFLHTNYSILKURWGGDNTCEXPYHTGPHSCHIPKD--- 163

Qy 178 ARCVVHGAEEFNSQYRINTEVNPGLAS-TRLLDVSLSQSLRDPDPPGLRVESSVPGYPRRL 236
 Db 164 -----LALFPYEWATEAHLRGSSRSVDVLTLDLVVVTTDPPPYHVSRVGGLEDQL 216

Qy 237 RASWTPASWPCQPHFL--KFLQKRPQHDWSVTP-------AGLBEVITDAVA 285
 Db 217 SVRWVSP--PALKDFLQKAYQYIRLRYEDSVWDWKVYDDVSNQTSRCLLAGK-----P 266

Qy 286 GLPHAYVRSARDF---LDAGTWSTWS-PEA-----WGTPTSGTI 320
 Db 267 GIVYFWVRCNFGITGSKRAGIWSMWSHPTAASTPRSERPGGGACEPRGEPPSSGPV 326

Qy 321 PKEIP--ANGOLH 331
 Db 327 RRELKQFLGNLKHK 340

RESULT 11
 US-09-880-578-24
 ; Sequence 24, Application US/09880578
 ; Patent No. US2002004573A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, Si
 ; Presneil, Scott R.
 ; Gilbert, Anna C.
 ; Foster, Donald C.
 ; Adams, Robyn L.

TITLE OF INVENTION: MAMMALIAN ZCYTORS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: ZymoGenetics
 STREET: 1201 Eastlake Ave East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102

TITLE OF INVENTION: MAMMALIAN ZCYTORS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: ZymoGenetics
 STREET: 1201 Eastlake Ave East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA

ZIP: 98102
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSQL for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/880,578
 FILING DATE: 13-Jun-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G.
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 96-22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 389 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 24:
 US-09-880-578-24

Query Match 9.3%; Score 211.5; DB 10; Length 389;
 Best Local Similarity 23.8%; Pred. No. 3.5e-07; Indels 95; Gaps 19;
 Matches 89; Conservative 53; Mismatches 137; InDelS 95; Gaps 19;

QY 17 TALVASSPCPQANGPPGVQYQGPGRSYVKLC-----PGVTAGDPVSWFRIDGE---PKL 67
 Db 3 TAVISPQDPTLLI-----GSSLLATCSVHGDPPGATA-EGLYWTLNGRRLPEL 50

QY 68 LOGQDSGLGHLVLAQD----STDEGTYICOTLDGAIGGTVLQLQYPPARPV-VSCQ 121
 Db 51 SRVLNAs---TIALALANINGSRORGNLVCHARDGSTLAGSCLYVLPKXPVNISCW 107

QY 122 AADYENFSCTWSPSQ---ISGLPTRYLTSYRKTKVYLGADSQRSPSTGPWPC--PQDPLGA 177
 Db 108 SKNMKDLICRWTPOSQHGETFLHNYSLKRYQGDTTCVEHTVGHSHCIPKD----163

QY 178 ARCVVHGAEEFWQSQRINTVEVNPGL-ASTRLLDVLSOSILRPDPQQLRVESYPGYPRRL 236
 Db 164 -----LALFTPEIWTEATNRIGSARDVTLIDLVVTDPPPDVHVSVRGGLEDQL 216

QY 237 RASITYPAWSPCOPFHLL-KFRLQYRAQHPAWSTVPB-----AGLEEVITDAV 285
 Db 217 SVRNNSP---PAALKDFLQAKYQTRYRVEDSVDWKVDDNOTSCRLAGLK-----P 266

QY 286 GLPHAVRYSARDF----LDASTWSTWS-PEA-----WGTTPSTGTI 320
 Db 267 GTVYFVQRCNPPIGYGSRKAGIWSEWHSPTAASTPRSERGEPRGGACEPRGEPSGPV 326

QY 321 PKEIP---AWGQHL 331
 Db 327 RRELKQFLGWLKHH 340

RESULT 12
 US-09-880-578-29
 Sequence 29, Application US/09880578
 Patent No. US20020045733A1
 GENERAL INFORMATION:
 APPLICANT: Lok, Si
 Presnell, Scott R.
 Jelberg, Anna C.
 Gilbert, Teresa

QY 286 GLPHAVRYSARDF----LDASTWSTWS-PEA-----WGTTPSTGTI 320
 Db 267 GTVYFVQRCNPPIGYGSRKAGIWSEWHSPTAASTPRSERGEPRGGACEPRGEPSGPV 326

QY 321 PKEIP---AWGQHL 331
 Db 327 RRELKQFLGWLKHH 340

RESULT 12
 US-09-880-578-29
 Sequence 29, Application US/09880578
 Patent No. US20020045733A1
 GENERAL INFORMATION:
 APPLICANT: Lok, Si
 Presnell, Scott R.
 Jelberg, Anna C.
 Gilbert, Teresa

RESULT 13
 Sequence 44, Application US/09037657A
 Patent No. US2002004574A1

GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Botstein, David
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kjavian, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FILE REFERENCE: P2548PCL

CURRENT APPLICATION NUMBER: US/09/944,413
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/067,411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
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 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090

RESULT 14
 US-09-944-413-32
 ; Sequence 32, Application US/09944413
 ; Patent No. US2002156004A1

PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. US002015600A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: No. US202015600A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999
 PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO: 32
 LENGTH: 422
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-09-944-413-32

Query Match 9.3% Score 211.5 DB 9 Length 422;
 Best Local Similarity 23.7% Pred. No. 3 9e-07
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QY 113 PARPY-VSQQADEVNFSCTWSPQ--ISGLPPRPLTSYRKIVLGADSQRSPSTGWPW 169
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QY 170 C-PQDPLGAARCVBHGAEFWSSOYRINTEVNPLG-ASTRLDVSLSILRPDPPQQLRV 226
 Db 195 CHIPKD-----LALFTPEIWEATNRGSAKSVDLTDILDVVTPDPPDVHV 243

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QY 276 LEEVITDAVGLPHAVRSARDF----LDAQTWSTWS-PEA-----311

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QY 312 -WGTPTSTGTIPKEP---AWGOLH 331
 Db 354 RGGPSSGPVREIKQFLQWLKKH 377

APPLICANT: Ferrara, Napooleone
 APPLICANT: Fivarooff, Ellen
 APPLICANT: Gerritsen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gunn, Austin
 APPLICANT: Hillian, Kenneth
 APPLICANT: Klayvin, Ivar
 APPLICANT: Napier, Mary
 APPLICANT: Roy, Margaret
 APPLICANT: Tunas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P2548P1C1
 CURRENT APPLICATION NUMBER: US/09/944,403
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/067,411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
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 PRIOR APPLICATION NUMBER: 60/069,278
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 PRIOR FILING DATE: December 12, 1997
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 PRIOR FILING DATE: December 16, 1997
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 PRIOR APPLICATION NUMBER: 60/069,870
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 PRIOR APPLICATION NUMBER: 60/068,017
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 PRIOR FILING DATE: February 9, 1998
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 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
 PRIOR APPLICATION NUMBER: PCT/US98/19330
 PRIOR FILING DATE: September 16, 1998
 PRIOR APPLICATION NUMBER: PCT/US98/25108
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: No. US2002016513A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313

RESULT 15
 US-09-944-403-32
 Sequence 32, Application US/09944403
 Patent No. US2002016513A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Eaton, Dan

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; PRIORITY FILING DATE: NO. US20020165143Aember 30, 1999
; PRIORITY APPLICATION NUMBER: PCT/US99/28301
; PRIORITY FILING DATE: December 1, 1999
; PRIORITY APPLICATION NUMBER: PCT/US99/30095
; PRIORITY FILING DATE: December 16, 1999
; PRIORITY APPLICATION NUMBER: PCT/US00/03565
; PRIORITY FILING DATE: February 11, 2000
; PRIORITY APPLICATION NUMBER: PCT/US00/04414
; PRIORITY FILING DATE: February 22, 2000
; PRIORITY APPLICATION NUMBER: PCT/US00/03841
; PRIORITY FILING DATE: March 2, 2000
; PRIORITY APPLICATION NUMBER: PCT/US00/08439
; PRIORITY FILING DATE: March 30, 2000
; PRIORITY APPLICATION NUMBER: PCT/US00/14042
; PRIORITY FILING DATE: May 22, 2000
; PRIORITY APPLICATION NUMBER: PCT/US00/20710
; PRIORITY FILING DATE: July 28, 2000
; PRIORITY APPLICATION NUMBER: PCT/US00/32678
; PRIORITY FILING DATE: December 1, 2000
; PRIORITY APPLICATION NUMBER: PCT/US01/05520
; PRIORITY FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO: 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-03-32

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Query Match          9.38;  Score 211.5;  DB 9;  Length 422;
Best Local Similarity 23.7%;  Pred. No. 3.9e-07;
Matches 91;  Conservative 53;  Mismatches 145;  Indels 95;  Gaps 19;
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Db   30 GAPRAGSGHTAVISQDPTLLI-----OSSLATCSCVHGDPDATA-BGLYWT 77
Qy   61 RDGE--PKLQGPDSGLGHIELVLAQAD----STDEGTYCOTLDGAEGTVTQLGYP 112
Db   78 LNRRRLPPSERVLNAs---TLALALANLNSQRSGDNVCHARDGSTLAGSCLYYVGLP 134
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Qy   170 C--PQDPLGAARCTVYHGAEFWSQYRINVTVEVNPLG - ASTRLRDVSLOSLRPDPQGLRV 226
Db  195 CHIPKD-----LAFTPYEWATEVNRLGSARSVDLTDLDVVTTDPPDVHV 243
Qy   227 ESVPGYPRRLRASWTPASNPQCPHFL - KFRLQYRPQHPAWSTVEP-----AG 275
Db  244 SRVGGLEDQLSVRWVSP---PAKDFLFQARYQIRYRVEDSDWKVDDVSNOTSCRLAG 300
Qy   276 LEEVITDAVAGLPHAVRVSADF---LDAQTWSWS-DEA----- 311
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Db  354 RGEPSSGPVRELKOFGLWKKH 377

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Search completed: January 17, 2003, 19:40:18
Job time : 17 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 19:36:45 ; Search time 18 Seconds
(without alignments)
689.804 Million cell updates/sec

Title: US-09-924-338-2
Perfect score: 2275
Sequence: 1 MSSSSGGLSRVLYAVATALV.....KPGFLASVIPVDRPGAPNL 422

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2275	100.0	422	4	US-08-929-846-2	Sequence 2, Appli
3	2257.5	99.2	423	4	US-08-702-665A-5	Sequence 5, Appli
4	1897	83.4	432	4	US-08-702-665A-3	Sequence 3, Appli
5	1831	80.5	441	4	US-09-151-102-4	Sequence 4, Appli
6	1831	80.5	441	4	US-08-929-846-4	Sequence 4, Appli
7	379	16.8	372	4	US-09-211-590-2	Sequence 2, Appli
8	379	16.7	372	1	US-07-865-878A-4	Sequence 4, Appli
9	379	16.7	372	1	US-07-676-647-2	Sequence 2, Appli
10	379	16.7	372	2	US-08-449-329-2	Sequence 2, Appli
11	379	16.7	372	2	US-08-445-073-2	Sequence 2, Appli
12	379	16.7	372	2	US-08-585-258-2	Sequence 2, Appli
13	379	16.7	372	2	US-08-603-110-2	Sequence 2, Appli
14	379	16.7	372	5	PCT-091-03896-2	Sequence 5, Appli
15	360	15.8	468	4	US-08-795-473B-5	Sequence 5, Appli
16	360	15.8	468	4	US-09-39-856-5	Patent No. 5171840
17	360	15.8	468	6	5171840-2	Patent No. 5171840
18	360	15.8	468	6	5480796-2	Patent No. 5171840
19	330	14.5	344	6	5171840-7	Patent No. 5171840
20	330	14.5	344	6	5480796-7	Patent No. 5171840
21	325	14.3	323	6	5171840-6	Patent No. 5171840
22	325	14.3	323	6	5480796-6	Patent No. 5171840
23	259.5	11.4	229	2	US-08-684-687-2	Sequence 2, Appli
24	259.5	11.4	229	3	US-08-352-678-6	Sequence 6, Appli
25	255.5	11.2	229	1	US-08-383-750-6	Sequence 6, Appli
26	240	10.5	230	5	PCT-US93-09636-6	Patent No. 5171840
27	232	10.2	386	6	5171840-5	Patent No. 5171840

ALIGNMENTS

RESULT 1
US-09-151-102-2
; Sequence 2, Application US/09151102
; Patent No. 6274447
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLUKEIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/151.102
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/663,584
; FILING DATE: 14-JUN-1996
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G12525
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5551
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-151-102-2

Query Match Score 2275; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 1,4e-173;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSSSGGLSRVLYAVATALVASSPCP0AWGPPGVQYGPGRSVKLCCPGVTAGDPWSWF 60
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RESULT 2
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Sequence 2, Application US/08929846
; Paten No. 630855
GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLUKEIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929, 846
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/663, 584
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32, 724
TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;

RESULT 3
US-08-929-846-5
Sequence 5, Application US/08702665A
; Patent No. 6274708
; GENERAL INFORMATION:
; APPLICANT: Hilton, Douglas J.
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702, 665A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19, 827
; REFERENCE/DOCKET NUMBER: 1,0296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.0%; Pred. No. 1-4e-173;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MSSSGSGLSRVLYAVATALYSASSPCPQAWGPPGYQGRSRVKLCPCGTAGDPVSNF 60
Qy 61 RDGEPKLQLQGPDGSGLGHELVLAQDSTDGTYTCOTLDGAGGTVTLQJGYPARPVSC 120
Db 61 RDGEPKLQLQGPDGSGLGHELVLAQDSTDGTYTCOTLDGAGGTVTLQJGYPARPVSC 120
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Db 181 VVHGAEEFWSSYRINTEVPLQLRPPQGLRVEVPGYPRRLASW 240
Qy 241 TYPASWPCQPHFLKFRQLQYRAQHPANSTVEPAGLEEVITDAVGLPHAVRYSAARDLD 300
Db 241 TYPASWPCQPHFLKFRQLQYRAQHPANSTVEPAGLEEVITDAVGLPHAVRYSAARDLD 300
Qy 301 AGTGSTWSPEAWGTPSTGTIPKEPAWGOLHTQPEVEQVDSPAPPRPSLQPHPRLDHR 360
Db 301 AGTGSTWSPEAWGTPSTGTIPKEPAWGOLHTQPEVEQVDSPAPPRPSLQPHPRLDHR 360
Qy 361 DSVEQVAVLASIGLSFLGLVAGALAGLWLRLRGKDGSKRPGFLASVIVYDRRGAP 420
Db 361 DSVEQVAVLASIGLSFLGLVAGALAGLWLRLRGKDGSKRPGFLASVIVYDRRGAP 420
Qy 421 NL 422
Db 421 NL 422


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FILING DATE: 14-JUN-1996
APPLICANT: Scott A. Brown
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8324
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-151-102-4

Query Match Score 80.5%; Length 441;
Best Local Similarity 83.1%; DB 4; Length 441;
Matches 340; Conservative 183.1%; Pred. No. 3.6e-138; Gaps 1;
Mismatches 17; Indels 2; Gaps 1;

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Qy 76 GHELYLAQADSTDEGYICOTLDGAGGTWTQLQGYPPARPVSCQAADYENFSCTWSPS 135
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Qy 196 TEVNPLGASTRLDVLSLQLSRLPDPDQGLRVEVSPGYPRRLRASWTPASWCPQPHELLK 255
Db 205 TEVNPLGASTCLLDYRLQSLIPDQGLRVEVSPGYPRRLRASWTPASWCPQPHELLK 264

Qy 256 FRQYRPAQHPAWSVTEPAGLEEVTIDAVGLPHAVRYSAARDFLDAGTWSWSPEANGTP 315
Db 265 FRQYRPAQHPAWSVTEPAGLEEVTIDAVGLPHAVRYSAARDFLDAGTWSWSPEANGTP 324

Qy 316 STGTPKEPAWGLHTQ - PEVPEQVQDSAPPAPPSLQPHPRLLHDROSEVQAVLASLG 373
Db 325 STGQLQDEIPDWQSQHGQGLEAVVAQEDSAPPAPRSQDPPRDLHDROLEQVAVLASLG 384

Qy 374 ILSPIGLVAGALAUGLWLRLRGKDGSPKGFLASVIFVDRPGAPNL 422
Db 385 IFSCLGLAVGALAUGLWLRLRGKDGFPQKLAPMIPVEKLPGIPNL 433

RESULT 6
US-08-929-846-4
; Sequence 4, Application US/08929846
; Patent No. 6,350895
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLUKEIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridge Park Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,846

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; FILING DATE: ; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,584
; FILING DATE: 14-JUN-1996
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5255
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-929-846-4

Query Match 80.5%; Score 1831; DB 4; Length 441;
Best Local Similarity 83.1%; Pred. No. 3.6e-138; 1;
Matches 340; Conservative 17; Mismatches 50; Indels 2; Gaps 1;

Qy 16 ATALVASSPCPQAWPQGPVQGPGRSVKLCPGVTAGDPVSMERDGPQLLQGPDSGL 75
Db 25 ATALVSSSPCQAWGPQVQGPGRVMLCCPGVS&gt;PVSFRDGDSRLQGPDSGL 84

Qy 76 GHRLVAQADSTDEGTYTCQTLGDALGGTVTOLGYPPARPVYSCQAAODYENFSCTWSPS 135
Db 85 GHRLVAQDVSDDEGTYVCQTLGDVGSG&gt;VLQFPARPEVSCQAVDYEENFSCTWSPG 144

Qy 136 QISGLPTRYLTYSRKTVLGADSQRSSPSTGMPQCPQDPDGAACRVVHAGFMHQYRINV 195
Db 145 QVSGLPTRYLTYSRKTVLGASQRESEPTGMPWCPQPQPLEASRCVVIGAEFFSEYRINV 204

Qy 196 TEVNPLGASTCLIDVRLQSLIPLDPPGQLRVEVPGPYPRRLRASWTPASWCPQPHFLK 255
Db 205 TEVNPLGASTCLIDVRLQSLIPLDPPGQLRVEVPGPYPRRLRASWTPASWRRQPHFLK 264

Qy 256 FRQYRPAQHPAWSTYEPAGLEEVITDAVAGLPHAVRVSARDFLDAGTWSTWSPEAWGTP 315
Db 265 FRQYRPAQHPAWSTYEPIGLEEVITDAVAGLPHAVRVSARDFLDAGTWASNSPEAWGTP 324

Qy 316 STGTIPKEIPAWGQLHTQ - PEVEQVQDSPAAPRPSLQPHPRLLDHRDSVEQAVLASLG 373
Db 325 STGQPLQDEIPWNSQGHGQQQLEAVQAQDSPAAPRPSLQPDPRLDHRDPLQEAVLASLG 384

Qy 374 ILSFLGLVAGALALGWLRLRGKGDSKPQGFLASVYIPDRPQGPAPNL 422
Db 385 IFSCGLGLAVGALALGWLRLRGKGDPQPKOLLAPMIVKLPGPINL 433

RESULT 7
US-08-211-590-2
; Sequence 2, Application US/09211590
; Patent No. 6316206
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Furth, Mark E.
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

```


APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/676,647
FILING DATE: 1991/03/28
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
-07-676-647-

RESULT 11
 US-08-445-073-2
 Sequence 2, Application US/08445073
 Patent No. 5819897
 GENERAL INFORMATION:
 APPLICANT: Davis, Samuel L.
 APPLICANT: Squinto, Stephen P.
 APPLICANT: Furth, Mark E.
 APPLICANT: Vancopoulos, George D.
 TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/445,073
 FILING DATE: 07/07/1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/676,647
 FILING DATE: 28-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 6526-048
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212 730-9030
 TELEFAX: 212 8698864/3741
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 372 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-445-073-2

Query Match 16.7%; Score 379, DB 2; Length 372;
 Best Local Similarity 30.1%; Pred. No. 1.5e-22;
 Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

Oy	12	LVAATPAVLVASSPCCPQAWGPGVQYQGPQRPSVKICPGVAGDPVSWRDGPBKLLQGP	71
Oy	12	: : : : : : : : : : : : :	71
Db	12	VLAARAVVVAQQRHSPQE - APHYQERLQSDVTLPCGTANWDAVTRVNGED - - LAP	66
Db	67	DLLNGSOLVGLGLEGHSGJACFPCGKSLQSLRHOVLLAHGPRLPPRVPSRSNTYPKGFY	126
Oy	130	CTWSPSQISQLPT * RYLTSPRKTKTILGADSQRSPSTGWPWCPDPLIGARCVVHGAFW	188
Db	127	CSWH-----LPTPVYIPNTFNVTWLHGSK-----IMCVERDPALKNRCHTRYMFL	172
Oy	189	S - QYININVTEVNPLGASTRLDYLSQLSTLRDPQQGLRVEVPGYPRRLRASWTYPSW	246
Db	173	STIKRVSISNSNAGHNRAITPSEFTWKPDPPENVARYPSNPRLPEVWTQTPSTW	232
Oy	247	PCQPHFLKFLQYRPAHQPAWSTYEP-A-GLEEVITDAYGLPHAVRYSARDFLDAGTWS	305
Db	233	PDPESPFLPKRQYRPLIDOWOHVYELSDTAHTLTDAYKEVTOIAAKD - NEIGTWS	291
Oy	306	TWSPEWAGTGTTSTGTPKEIAPMGLQHTQPVEPYDSDPAPRPSLQPHPRLDHRDSVEQ	365

Db 292 DWSVAHAATPWTTE-PRHLTEAQ--AAETTTSSTSSLIAPP---PTTKICD----- 332
 ; Sequence 2, Application US/08585258
 ; Patent No. 589,003
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, Samuel
 ; APPLICANT: Squinto, Stephen P.
 ; APPLICANT: Furth, Mark E.
 ; APPLICANT: Yancopoulos, George D.
 ; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/585,258
 ; FILING DATE: 11-JAN-1996
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/001,904
 ; FILING DATE:
 ; APPLICATION NUMBER: US/07/700,677
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 6526-065
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 869 9090
 ; TELEFAX: 212 8698854/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 372 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US - 08 - 585 - 258 - 2

Query Match 16.7%; Score 379; DB 2; Length 372;
 Best Local Similarity 30.1%; Pred. No. 1.5e-22;
 Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 71

Qy 12 LVAVATAVLVASSQSPDQAWGDPGVQNGQPGRSVWKLCCPGVTLQGDPVSKERDGEPKLLQGP 71
 ::| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
 12 VLAAGAAAVYQQRHSQE- -APHQVQERLGSVNTLPQGTANWDAAVTRWRVNGTD--LAP 66

Qy 72 DSGLGHELVLAQADSDTEGTYTCOTLDG-ALGGTVTLQLGYPARPVSYCQAADY-ENFS 129
 | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
 67 DLLNSQVLGVGLHEHSGLYACFIRDWSHLRHOVLHVGLPQREPVSLSRSTYTPCFY 126

Qy 130 CTWPSOISGLPT-RYLTYSRKTKTIVLGADSQRRSRSPSTGWPWPQDPLGAARCVHGAEFW 188
 | :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
 Db 127 CSWH----LPTNFVTVLHGSK-----IMVCEKDPAKRNCHRYMHLF 172

Qy 189 S-QFIVNTEVNPLGASTRLDVDSLOSILRPDPQGRVESVGPYPRRLRASWTPASW 246

Db 173 STIKYKYSISVNALGHNATAITDEFTIVKDPENNVAAPVPSNPRRLTEWTQTPSTW 232
 Qy 247 PCOPHFLKFRILQYRPAQHAWMASTVEPA -GLEEVITDAAGLPHAYRVSAARDFLDAGTWS 305
 Db 233 PDEPSFLPKFRYLPLDQMQHVELSDTGTAHTIDAYAKEYTIIQVAAD -NEIGTWS 291
 Qy 306 TWSPEANGTPSTGTIPKEIPAWGQLHTQPEYEQVQDSPAPRPSLQPHPRLLDHDRSVEQ 365
 Db 292 DMSVAARATPWTEE -PRLHTEAQ -AAETTSTTSSSLAP -PTTKICD-----
 Qy 366 VAVLASIGLISFLGLVAGALALGLWLRLRQGKDGSPKGFLASH 410
 Db 337 ----- PGEL ----- GSGGGPCAPLVSV 354

RESULT 13
 US-08-603-010-4
 ; Sequence 4 , Application US/08603010
 ; Patent No. 5955290
 ; GENERAL INFORMATION:
 ; APPLICANT: Yancopoulos, George D. et al.
 ; TITLE OF INVENTION: Cell Free Ciliary Neurotrophic Factor/Receptor Complex
 ; NUMBER OF SEQUENCES: 6
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/603,010
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/118,968
 ; FILING DATE: 09-SEP-1993
 ; APPLICATION NUMBER: US 07/801,562
 ; FILING DATE: 02-DEC-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 6326-082
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9090
 ; TELEX: 66141 PENNIE 4 :
 ; INFORMATION FOR SEQ ID NO: 4 :
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 372 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-603-010-4

Query Match 16.7%; Score 379; DB 2; Length 372;
 Best Local Similarity 30.1%; Pred. No. 1.5e-22;
 Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

Db 12 LIVAVATALYSASSPQPQANGPPGYQGDPGRSVKLCCPGVYTAGDPVSFRDGEPKLLOGP 71
 Db 12 VLAAAAYVYVQRHSPQE -APHYQYERLGSDVTLPCTANWDAAVTWYNGTD -- LAP 66
 Qy 72 DSGLGEHLVIAQASDTEGTYICQFLDG -ALGIVGTVLQGYPPARPVVSCQAADY -ENFS 129
 Db 67 DLINSQLVVLHGLELGHSGLYACFHRDSWHLRHQVLLHVGLPPREVLSCRNTYPKGFY 126

Qy 130 CTWSPSSQISGLPT -RYLTSYRKKTVLOADSQRSPSSTGPWPCPQDBGAARCVVHGAEFW 188
 Db 127 CSWH ----- LPRTPTYLPNTENVTVLHSK ----- IMCEKPAALKHCHIRYMHFL 172
 Qy 189 S -QYRINVTEVNPLGASTRLDVSLQSILRPDPOGLRVESVPGYPRRLRASVTPASW 246
 Db 173 STIKYKYSISVNALGHNATAITDEFTIVKDPENNVARPVPNSPRLLEVTWQTPSTW 232
 Qy 247 PCOPHFLKFRILQYRPAQHAWMASTVEPA -GLEEVITDAAGLPHAYRVSAARDFLDAGTWS 305
 Db 233 PDPESEFLKEFYRPLDQWQHVEISDGTAAHTIDAYAKEYTIIQVAAD -NEIGTWS 291
 Qy 306 TWSPEANGTPSTGTIPKEIPAWGQLHTQPEYEQVQDSPAPRPSLQPHPRLLDHDRSVEQ 365
 Db 292 DWVAAAHATPATEE -RHLTEAQ -AAETTSTTSSSLAPP ----- PTTKICD----- 336
 Qy 366 VAVLASIGLISFLGLVAGALALGLWLRLRQGKDGSPKGFLASH 410
 Db 337 ----- PGEL ----- GSGGGPCAPLVSV 354

RESULT 14
 PCT-US91-03896-2
 ; Sequence 2 , Application PC/TUS9103896
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, Samuel E.
 ; APPLICANT: Squinto, Stephen P.
 ; APPLICANT: Furth, Mark E.
 ; APPLICANT: Yancopoulos, George D.
 ; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/03896
 ; FILING DATE: 1991-06-03
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 6526-065-228
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9090
 ; TELEX: 66141 PENNIE 4 :
 ; INFORMATION FOR SEQ ID NO: 2 :
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 372 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; PCT-US91-03896-2

Query Match 16.7%; Score 379; DB 5; Length 372;
 Best Local Similarity 30.1%; Pred. No. 1.5e-22;
 Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

Qy 12 LIVAVATALYSASSPQPQANGPPGYQGDPGRSVKLCCPGVYTAGDPVSFRDGEPKLLOGP 71
 Db 12 VLAAAAYVYVQRHSPQE -APHYQYERLGSDVTLPCTANWDAAVTWYNGTD -- LAP 66
 Qy 72 DSGLGEHLVIAQASDTEGTYICQFLDG -ALGIVGTVLQGYPPARPVVSCQAADY -ENFS 129
 Db 67 DLINSQLVVLHGLELGHSGLYACFHRDSWHLRHQVLLHVGLPPREVLSCRNTYPKGFY 126
 Qy 72 DSGLGEHLVIAQASDTEGTYICQFLDG -ALGIVGTVLQGYPPARPVVSCQAADY -ENFS 129

RESULT 15
 US-08-795-473B-5
 ; Sequence 5 , Application US/08795473B
 ; Patent No. 6237858

GENERAL INFORMATION:
 / APPLICANT: Galun, Ethan
 / APPLICANT: Nahot, Orit
 / APPLICANT: Blum, Herbert E.
 / TITLE OF INVENTION: A Pharmaceutical Composition for Treating
 / NUMBER OF SEQUENCES: 10
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Davidson, Davidson and Kappel, LLC
 / STREET: 1140 Avenue of the Americas
 / CITY: New York
 / STATE: New York
 / COUNTRY: USA
 / ZIP: 10036

COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.5 inch disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: MS-DOS EDITOR
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/795,473B
 / FILING DATE: 11-FEB-1997
 / CLASSIFICATION:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Davidson, Clifford M.
 / REGISTRATION NUMBER: 32,728
 / REFERENCE/DOCKET NUMBER: 963-1.1007
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (212)-997-1028
 / TELEFAX: (212)-997-1037
 / INFORMATION FOR SEQ ID NO: 5:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 468 amino acids
 / TYPE: amino acid
 / TOPOLOGY: unknown
 / US-08-795-473B-5

Query Match 15.8%; Score 360; DB 4; Length 468;
 Best Local Similarity 28.4%; Pred. No. 6.6e-21;
 Matches 129; Conservative 57; Mismatches 196; Indels 72; Gaps 19;

Qy 1 MSSCCSLSRLVVALAVATLYASSPQPQANGPPGYOQGRSVYKCCPQVTAGD-PVS 58
 Db 2 LAVGCALLAALIAAPSAAL-APRRCPAQEVARGVILTSLLSDSVTLTCPGVEPEDNATVH 59
 Qy 59 WERDGEPKLQGPD-----SGLGHELLVLAQADSTDEETYICQTDLGALGGTVTQLG 110

Db 60 w-----VLRKPAAGSHPSRAGMCRRLRLRSVOLHDSGNNSCYRA-GRPAGTVHLVD 111
 Qy 111 YPPARPVSC-QAADYENFSCTWSQSPQISGLPTRYLTSYRKKTVLGADSORRSRSPSTG-PW 168
 Db 112 VPPEEEQPLCSRKSPLSNVYCCEWGPSPSTSLLT-----KAVLVRKQNSPAEDFQE 163
 Qy 169 PC---PQDPLGAARCVHGAEEFWNSRINTEVNPLGAS-TRILLVLSLOSSILRDPQQG 223
 Db 164 PCQYSQESOKESQFLCOLAVPEGDS-SYIVTSMCVAASSVGSKFSKTQTFQGGILQDPDPAN 221
 Qy 224 LRVESYPGYPPLRASWTYPASWPCCOPHFLKFRLQYRPQAHPAHNTVEPAGLEE-VIT 281
 Db 222 ITVTAVARNPRWLSSVWQDPHSWN-SSFYRLRFELRYRAERSKTTWMMVKDLQHHCVIH 280
 Qy 282 DAVAGLPHAVYRSARFLDAQTWSIISPEAMGTSPNGTIPKEIPAMGQLHTQPEVYEPQVD 341
 Db 281 DAWSGLRHVYVOLRAQEFQGQEWSEWSPEAMGTPTWES-----RSPPANEVS 328
 Qy 342 SPAPPRLSLOPHPRLDHRSVEQAV----LASLGLSFLGVLVAGALA LG-----388
 Db 329 TPMQALTTNKDDNII-FRDSANATLIPVQDSSSYVLPFTL-VAGGSLLAFGTLLCIAIVL 386
 Qy 389 ---LW-LRLRRGGKGDKSPKPGFLASVTPYDRRP 417
 Db 387 REFKTKWKLRALEGKTSMHPPYSLGGLVPERPRP 420

Search completed: January 17, 2003, 19:39:29
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GenCore version 5.1.3								
Copyright (c) 1993 - 2003 Compugen Ltd.								
OM protein - protein search, using sw model								
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Perfect score:	227/500 seqs, 133250620 residues							
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	Gapopen 10.0 , Gapext 0.5							
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Total number of hits satisfying chosen parameters:	908470							
Minimum DB seq length:	0							
Maximum DB seq length:	2000000000							
Post-processing:	Minimum Match 0%, Maximum Match 100%							
	Listing first 45 summaries							
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	22: /SIDS2/godata/geneseq/geneseqp-emb1/AA2001.DAT:*							
	23: /SIDS2/godata/geneseq/geneseqp-emb1/AA2002.DAT:*							
Pred. No.	is the number of results predicted by chance to have a higher score than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
	SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	Description			
1	2275	100 0	422	17	AAR9090	Human interleukin-		
2	2275	100 0	422	22	AAB3654	Human IL-11 receptor		
3	2275	100 0	422	22	AAU0725	Human interleukin-		
4	2275	100 0	422	23	AAE14613	Human interleukin-		
5	2275.5	99.2	423	17	AAR92814	Murine interleukin-		
6	1897	83.4	432	17	AAR92813	Murine interleukin-		
7	1871	82.2	432	22	AAB3653	Mouse IL-11 receptor		
8	1831	80.5	441	17	AAR9091	Murine Et1-2 gene		
9	1831	80.5	441	22	AAU0726	Mouse Et1-2		
10	1831	80.5	441	23	AAE14614	Murine Et1-2 prote		

PD	27-JUN-1996.	AC	AAB36654;
XX		XX	
PF	27 - NOV - 1995; 95WO-US15400.	DT	13-MAR-2001 (first entry)
XX		XX	
PR	22 - DEC - 1994; 94US-0362304.	DE	Human IL-11 receptor subunit alpha protein SEQ ID NO:11.
XX		XX	
PA	(GEMY) GENETICS INST INC.	KW	DNAX cytokine receptor subunit; DCRS2; receptor protein;
XX		KW	modulating cell proliferation; diagnosis; detection; drug screening;
PT	Tobin JF;	KW	immunological disorder.
XX		XX	
DR	WPI; 1996-30958B/31.	OS	Homo sapiens.
DR	N PSDK; AAT3278.	XX	
XX		PN	WO200073451-A1.
PR	New nucleic acid encoding human interleukin 11 receptor - and related protein, antibodies, receptor antagonists, etc, useful for treating and preventing loss of bone mass	XX	
PR		PD	07-DEC-2000.
XX		XX	
PS	Claim 13; Page 35-37; 54pp; English.	PF	30-MAY-2000; 2000WO-US14867.
XX		XX	
CC	Human interleukin-11 (IL-11) receptor (AAR99090) is thought to play a role in the regulation of bone maturation and repair. Its amino acid sequence was deduced from a cDNA clone (AT33278) isolated from a human activated peripheral blood mononuclear cell cDNA library.	PR	01-JUN-1999; 99US-0322913.
CC		XX	
CC	Recombinant IL-11 receptor or its fragments, pref. amino acids 24-422, 24-365 (soluble extracellular domain), 391-422, 102-422 or 102-365, can be expressed in host cell systems. It is used to treat/prevent loss of bone mass (e.g. osteoporosis, Paget's disease, multiple myeloma or hypogonadal conditions), as well as immune diseases and cancer.	PA	(SCHE) SCHERING CORP.
CC		PI	Dowling LM, Timans JC, Gorman DM, Kastlein RA, Bazan FU;
CC		XX	WPI; 2001-061536/07.
CC		XX	Novel composition comprising DNAX cytokine receptor subunit polypeptide useful for regulating immune system function and for treating immunological disorders -
CC		XX	Disclosure; Page 13-15; 93pp; English.
CC		PS	Sequence 422 AA;
XX		XX	Query Match 100.0%; Score 2275; DB 17; Length 422; Best Local Similarity 100.0%; Pred. No. 1_2e-150; Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MSSCAGSLSRVLYAVATALYSASSSPCPQAQWGPVGQYQGPGRSVKLCCPGVYTAGDPVSWF 60	Db	1 MSSCAGSLSRVLYAVATALYSASSSPCPQAQWGPVGQYQGPGRSVKLCCPGVYTAGDPVSWF 60
Qy	61 RDGEPKLQGPDGLGHLVLAQADSTDEGYICQTLDGAIGTVTQLGYPARPVSC 120	Db	61 RDGEPKLQGPDGLGHLVLAQADSTDEGYICQTLDGAIGTVTQLGYPARPVSC 120
Qy	121 QADYENFSCTWSPSQISGLPTRYLTSRKTVLQADSTDEGYICQTLDGAIGTVTQLGYPARPVSC 120	Db	121 QADYENFSCTWSPSQISGLPTRYLTSRKTVLQADSTDEGYICQTLDGAIGTVTQLGYPARPVSC 120
Qy	121 QADAEFNSCTWSPSQISGLPTRYLTSRKTVLQADSTDEGYICQTLDGAIGTVTQLGYPARPVSC 180	Db	121 QADAEFNSCTWSPSQISGLPTRYLTSRKTVLQADSTDEGYICQTLDGAIGTVTQLGYPARPVSC 180
Qy	181 VVHGAEEFSQYRINTVEVNPLGASTRLDLSQTLRDPDPPQGLRVEVPYPRRLRASW 240	Db	181 VVHGAEEFSQYRINTVEVNPLGASTRLDLSQTLRDPDPPQGLRVEVPYPRRLRASW 240
Qy	181 VVHGAEEFSQYRINTVEVNPLGASTRLDLSQTLRDPDPPQGLRVEVPYPRRLRASW 240	Db	181 VVHGAEEFSQYRINTVEVNPLGASTRLDLSQTLRDPDPPQGLRVEVPYPRRLRASW 240
Qy	241 TYPASWPCQPHFLKFRQLQYRPAQHPAWSTVPEAGLEEVITDAVGLPHAVRSARDFLD 300	Db	241 TYPASWPCQPHFLKFRQLQYRPAQHPAWSTVPEAGLEEVITDAVGLPHAVRSARDFLD 300
Qy	241 TYPASWPCQPHFLKFRQLQYRPAQHPAWSTVPEAGLEEVITDAVGLPHAVRSARDFLD 300	Db	241 TYPASWPCQPHFLKFRQLQYRPAQHPAWSTVPEAGLEEVITDAVGLPHAVRSARDFLD 300
Qy	301 AGTWSTWSPEAWGTPSTGTIPKEPAWQOLHTQPEVPOVDSPAPRPSLQPHPRLDHR 360	Db	301 AGTWSTWSPEAWGTPSTGTIPKEPAWQOLHTQPEVPOVDSPAPRPSLQPHPRLDHR 360
Qy	301 AGTWSTWSPEAWGTPSTGTIPKEPAWQOLHTQPEVPOVDSPAPRPSLQPHPRLDHR 360	Db	301 AGTWSTWSPEAWGTPSTGTIPKEPAWQOLHTQPEVPOVDSPAPRPSLQPHPRLDHR 360
Qy	361 DSVEQAVIALSGLGILSFLGLYVAGALALGMLRLRGKGKDQSPKPGFLASVTPVDRRGAP 420	Db	361 DSVEQAVIALSGLGILSFLGLYVAGALALGMLRLRGKGKDQSPKPGFLASVTPVDRRGAP 420
Qy	361 DSVEQAVIALSGLGILSFLGLYVAGALALGMLRLRGKGKDQSPKPGFLASVTPVDRRGAP 420	Db	361 DSVEQAVIALSGLGILSFLGLYVAGALALGMLRLRGKGKDQSPKPGFLASVTPVDRRGAP 420
Qy	421 NL 422	Db	421 NL 422
Qy	421 NL 422	Db	421 NL 422
Qy	241 TYPASWPCQPHFLKFRQLQYRPAQHPAWSTVPEAGLEEVITDAVGLPHAVRSARDFLD 300	Db	241 TYPASWPCQPHFLKFRQLQYRPAQHPAWSTVPEAGLEEVITDAVGLPHAVRSARDFLD 300
Qy	301 AGTWSTWSPEAWGTPSTGTIPKEPAWQOLHTQPEVPOVDSPAPRPSLQPHPRLDHR 360	Db	301 AGTWSTWSPEAWGTPSTGTIPKEPAWQOLHTQPEVPOVDSPAPRPSLQPHPRLDHR 360

Qy 361 DSVEQAVILASLGILSFLIGVAGALALGLWLRLRGKGDKGSPKPGFLASWYIPVDRRGAP 420
Db 361 DSVEQAVILASLGILSFLIGVAGALALGLWLRLRGKGDKGSPKPGFLASWYIPVDRRGAP 420
XX
Qy 421 NL 422
Db 421 NL 422

RESULT 3
AAU07725 ID AAU07725 standard; Protein; 422 AA.
XX
AC AAU07725;
XX DT 04-DEC-2001 (first entry)
XX DE Human interleukin 11 receptor, IL-11R.
XX KW Human; interleukin 11 receptor; IL-11R; cytosatic; antianaemic; anaemia;
KW osteopathia; leukopenia; bacterial infection; viral infection; anaemia;
KW B cell deficiency; T cell deficiency; haematopoietic cell deficiency;
KW bone marrow transplantation; immune deficiency; cancer; osteoporosis;
KW Paget's disease; multiple myeloma; hypogonadism.
XX OS Homo sapiens.
XX FH Key
FT Peptide 1..22
FT Peptide FT /label= "Signal_peptide"
FT Peptide 1..23
FT Peptide FT /label= "Signal_peptide"
FT Peptide 1..25
FT Peptide FT /label= "Signal_peptide"
FT Peptide 23..422
FT Protein FT /label= "Mature_IL-11R"
FT Domains FT /note= "Alternative mature protein"
FT Domains FT /label= "Immunoglobulin_like_domain"
FT Domains FT /label= "Extracellular_domain"
FT Domains FT /note= "This sequence is specifically claimed in
claim 1, this domain may start at residue 23"
FT Region FT /note= "This sequence is specifically claimed in
claim 1"
FT Region FT /note= "This sequence is specifically claimed in
claim 1"
FT Region FT /note= "This sequence is specifically claimed in
claim 1"
FT Protein FT /label= "Mature_IL-11R"
FT Protein FT /note= "Alternative mature protein"
FT Domains FT /label= "Mature_IL-11R"
FT Domains FT /note= "Alternative mature protein"
FT Domains FT /note= "This sequence is specifically claimed in
claim 2"
FT Domains FT /label= "Type_I_cytokine_domain"
FT Domains FT /label= "Transmembrane_domain"
FT Domains FT /label= "Intracellular_domain"

PD 14-AUG-2001.
XX XX
PF 10-SEP-1998; 98US-0151102.
XX XX
PR 14-JUN-1996; 96US-0663584.
PR 15-SEP-1997; 97US-0929846.
XX PA (GEMY) GENETICS INST INC.
XX
PI Tobin J;
XX DR WPI: 2001-549157/61.
DR N-PSDB; AS11970.

AC Binding inhibition of interleukin-11 to the human IL-11 receptor,
PT useful for treatment of anaemia comprises administration of a
PT composition containing a human IL-11R receptor protein comprising
PT specific amino acid sequence -
XX
PS Claim 1; Column 19-22; 19pp; English.
XX The invention relates to a method of inhibition binding of interleukin-11
CC (IL-11) to the human IL-11R receptor comprises administration of a
CC composition containing a human IL-11R receptor protein comprising an
CC amino acid sequence of 24-365, 102-365, 24-345 or 24-324 amino
CC acids of the human IL-11R protein sequence appearing as AAU07725. The
CC method is used for inhibiting binding of IL-11 to the human IL-11
CC receptor for the treatment of leukopenia, bacterial and viral
CC infections, anaemia, B cell or T cell deficiencies such as immune cell or
CC haematopoietic cell deficiency followed by bone marrow transplantation,
CC immune deficiency, cancer, regulation of bone maturation, and repair, bone
CC loss (including that associated with osteoporosis, post-menopausal
CC osteoporosis, senile osteoporosis, idiopathic osteoporosis, Paget's
CC disease, multiple myeloma and hypogonadal conditions). The present
XX sequence represents human IL-11R.
SQ Sequence 422 AA;

Query Match Score 2275; DB 22; Length 422;
Best Local Similarity 100.0%; Fred. No. 1.2e-150; Mismatches 0; Indels 0; Gaps 0;
Matches 422; Conservative 0; Gaps 0;

Qy 1 MSSSCSGLSLRSRVLYAVATLYSASSPQPQANGPPGVYQQGPGRSVKICCPGVTAGDPSWF 60
Db 1 MSSSCSGLSLRSRVLYAVATLYSASSPQPQANGPPGVYQQGPGRSVKICCPGVTAGDPSWF 60
Qy 1 RDGEPKLQLQGPDGSGLGHELVLAQADSTDEGYICQTLGALGGTIVTQLGYPPARFVSC 120
Db 1 RDGEPKLQLQGPDGSGLGHELVLAQADSTDEGYICQTLGALGGTIVTQLGYPPARFVSC 120
Qy 1 QAADYENFSCTWSPSQISGLPTRYLTSYRKTVLGAQDSQRSPSCTWPWPCQDPDPLGAARC 180
Db 121 QAADYENFSCTWSPSQISGLPTRYLTSYRKTVLGAQDSQRSPSCTWPWPCQDPDPLGAARC 180
Qy 181 VVHGAFFWSQRINVTYEVNPLGASTPLDLSQSLTRLPDPQGLAVESVPGYPRRLRASW 240
Db 121 VVHGAFFWSQRINVTYEVNPLGASTPLDLSQSLTRLPDPQGLAVESVPGYPRRLRASW 240
Qy 241 TYPASKPCQPHFLKERLQYPAQHAWSTVPEAGLEVITDAVLPHAVRVSARDFLD 300
Db 241 TYPASKPCQPHFLKERLQYPAQHAWSTVPEAGLEVITDAVLPHAVRVSARDFLD 300
Qy 301 AGTWSTWSPEAWGTPSTGTKEIPKAQGOLHTOPEVPOYDSPAPPRTSLOPHPRLLDHR 360
Db 301 AGTWSTWSPEAWGTPSTGTKEIPKAQGOLHTOPEVPOYDSPAPPRTSLOPHPRLLDHR 360
Qy 361 DSVEQAVLASLGILSFLGLYAGALALGNLWRKGDKGSPKPKFLASVTPDVRPGAP 420
Db 361 DSVEQAVLASLGILSFLGLYAGALALGNLWRKGDKGSPKPKFLASVTPDVRPGAP 420
Qy 421 NL 422
Db 421 NL 422

PN US6224547-B1.

RESULT 4	PI	Tobin J;
AAE14613	XX	
ID AAE14613 standard; Protein; 422 AA.	DR	WPI; 2002-215268/27.
XX	N-PSDB; AAD27928.	
AC AAE14613;	XX	
XX	PT	Novel isolated human interleukin-11 receptor protein useful in assays
AC to screen for binding agents and for treating immune deficiencies, cancer and bone related disorders, e.g., osteoporosis -	PT	
XX	PT	
DE 18-JUN-2002 (first entry)	PS	Claim 1; Column 19-22; 20pp; English.
DE Human interleukin-11 receptor.	XX	
XX	CC	The present sequence is human interleukin-11 receptor (IL-11R).
KW Human; interleukin-11; receptor; IL-11R; immune deficiency;	CC	IL-11R is involved in the regulation of immune system by interaction
KW haematopoietic progenitor cell; cancer; bone loss; osteoporosis;	CC	with IL-11. The IL-11R polypeptide may be used to screen for agents that
KW Paget's disease; multiple myeloma; hypogonadal condition.	CC	bind to it or interfere with the binding of IL-11, as diagnostic agent
XX	CC	for detecting the expression or presence of IL-11R, IL-11 or cells
OS Homo sapiens.	CC	expressing IL-11R or IL-11. The IL-11R and IL-11R inhibitors may be
XX	CC	useful in treatment or modulation of IL-11-related conditions which
Key Peptide	CC	include immune deficiencies, specifically deficiencies in hematopoietic
1..23	CC	progenitor cells, or related disorders, cancer and other diseases.
FT	CC	It is also believed that IL-11 and IL-11R may play a role in the
FT	CC	regulation of bone maturation and repair. As a result, human IL-11R
FT	CC	protein and IL-11R inhibitors may be useful in treatment of bone loss
FT	CC	(including that associated with osteoporosis, post-menopausal
FT	CC	osteoporosis, senile osteoporosis, idiopathic osteoporosis, Paget's
FT	CC	disease, multiple myeloma and hypogonadal conditions).
FT	XX	
FT	Sequence	422 AA;
Region	Query Match	100.0%; Score 2275;
FT	Best Local Similarity	100.0%; Pred No. 1.2e-150;
FT	Matches	422; Mismatches 0; Indels 0; Gaps 0;
Region	QY	1 MSSSCSGISRLVIVAYATLVASSSPCPAWGPICGVQKOPGRSVKLICCPGVTAGDPVSWF 60
FT	Db	1 MSSSCSGISRLVIVAYATLVASSSPCPAWGPICGVQKOPGRSVKLICCPGVTAGDPVSWF 60
Region	QY	61 RDGEPKLIQGPDGLGHLLVIAQADSTDBGTYCICQTLDGALGTVTVLQGYLPARPVSC 120
FT	Db	61 RDGEPKLIQGPDGLGHLLVIAQADSTDBGTYCICQTLDGALGTVTVLQGYLPARPVSC 120
FT	QY	121 QADDYENFSCTWSPQTSGLPHTYLTSRKTKTVLGADSQRSPSTGPMPCPDODPLGARC 180
Domain	Db	121 QADDYENFSCTWSPQTSGLPHTYLTSRKTKTVLGADSQRSPSTGPMPCPDODPLGARC 180
FT	QY	181 VVGAEEFWSQYRINVENTNPLGASTRLDVSLSQSLTPEAGLEHAVRSARFDLNSW 240
FT	Db	181 VVGAEEFWSQYRINVENTNPLGASTRLDVSLSQSLTPEAGLEHAVRSARFDLNSW 240
Region	QY	241 TYPASWPQPHFLKFRQLYRPAQHPAMSTVEPAGLEEVITDAVAGLPHAVRSARFDL 300
FT	Db	241 TYPASWPQPHFLKFRQLYRPAQHPAMSTVEPAGLEEVITDAVAGLPHAVRSARFDL 300
FT	QY	301 AGTWSWTPSPEANGTPSTGTPKEITPQMEVEPQVDSPAPPRLSQQHPRLLDHR 360
Domain	Db	301 AGTWSWTPSPEANGTPSTGTPKEITPQMEVEPQVDSPAPPRLSQQHPRLLDHR 360
FT	QY	361 DSVEQAVLASGILSPGFLIGYAGALAQLWLRLRGKDKGSPKPGFLIASVIEVDRRGAP 420
FT	Db	361 DSVEQAVLASGILSPGFLIGYAGALAQLWLRLRGKDKGSPKPGFLIASVIEVDRRGAP 420
XX	QY	421 NL 422
PN US6350055-B1.	DB	421 NL 422
XX	PD	26-FEB-2002.
XX	PF	15-SEP-1997; 97US-0929846.
XX	PR	14-JUN-1996; 96US-0663584.
XX	PR	22-DEC-1994; 94US-0362304.
XX	PA	(GEMY) GENETICS INST INC.
XX	PA	•XX
XX	XX	21-MAY-1996 (first entry)
XX	ID	RES92814
XX	AC	AAR92814;
XX	XX	
XX	DT	

CC	from adult mouse liver cDNA libraries. Nr1 is a low affinity receptor for IL-11 and interacts with gp130 to generate a high affinity IL-11 receptor. IL-11 can be used to develop agonists or antagonists of therapeutic apnl. or in the treatment or diagnosis of conditions involving a deficiency of IL-11, excess IL-11 or aberrant effects of normal endogenous IL-11	PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FU; XX WPI; 2001-061536/07.
CC	Novel composition comprising DNAX cytokine receptor subunit polypeptide useful for regulating immune system function and for treating immunological disorders -	PT PT PT XX
XX	Sequence 432 AA;	Disclosure; Page 13-15; 93pp; English.
Query	83.4%; Score 1897; DB 17; Length 432; Best Local Similarity 83.5%; Pred. No. 2.7e-124; Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1;	XX
Db	1 MSSSCSGLSRVLVAYATLYSASSSPCPOANCPGCVQYQGPGRSVKLCCPGVTAGDPVSWF 60 1 MSSSSGLSTRLVAYATLYSASSSPCPOANCPGCVQYQGPGRSVMLCCPGVSAGPVSWF 60	CC
Qy	61 RDGPKLLOGDGSGLCHELVIAQASDDEGYICOTLDGAAGGTWTLQGYPPARPVSC 120	CC
Db	61 RDGDSRLQDGSGLGHRLVLAQDSDPDEGVYVCQTLDGVSggMVLKLGFPAPRVEVSC 120	CC
Qy	121 QADYENFSCWWSPSQISGLFTRLYTSYRKTVLGDSORRSPSTGPWPWCPQDPGLAARC 180 121 QAVDYNENFSCWWSQVSGLFRTRLYTSYRKTLPAESQRESPTGPWPWCPQDPLEASRC	CC
Db	181 VVHGAEEFWSSOYRINTEVNPFLGASTRLDVSQSLTRDPPQPLRVESYPGYPRRLRASW 240 181 VVHGAEEFWSSOYRINTEVNPFLGASTRLDVSQSLTRDPPQPLRVESYPGYPRRLHASW	CC
Qy	241 TYPASWPCOPHELLKFRLQYRPAQHPAWSTVEPAGLEEVTDAGLPHAVRSARDFLD 300	CC
Db	241 TYPASWRCOPHELLKFRLQYRPAQHPAWSTVEPAGLEEVTDAGLPHAVRSARDFLD 300	CC
Qy	301 AGTWSWTPSPEAWGTPSTGT1KEPAWGLHTQ - PEVEPQVDSPAPPSPLOPHPRLLD 358 301 AGTWSWTPSPEAWGTPSTGT1QDEPDWSSGHHQGLEAVVAQEDSPAPPSPLOQDPRPID 360	CC
Db	359 HRDSEVOQAVLASIGLISLFLGIVAGALGLWLRLRGKGDKGSPKPGFLASV1PVDRPG 418 361 HRDPLEQVAVLASIGLISLFLGIVAGALGLWLRLRGKGDKGSPKPGFLASV1PVDRPG 420	CC
Qy	419 APNL 422	CC
Db	421 IPNL 424	CC
RESULT 7	Mus sp.	RESULT 8
AAB3653	standard; protein; 432 AA.	AAR99091 standard; protein; 441 AA.
X	ID AAB36653	ID AAR99091;
X	AC AAB36653;	AC AAR99091;
X	DT 13-MAR-2001 (first entry)	XX DT 09-OCT-1996 (first entry)
X	DE Mouse IL-11 receptor subunit alpha protein SEQ ID NO:10.	DE Murine Et1 -2 gene product.
X	KW DNAX cytokine receptor subunit; DCRS2; receptor protein; modulating cell proliferation; diagnosis; detection; drug screening; immunological disorder.	KW Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone; myeloma; Et1-2.
OS	OS	XX KW osteoporosis; Paget disease; myeloma; XX
PN	PN WO200073451-A1.	XX
XX	PD 07-DEC-2000.	XX
XX	PF 30-MAY-2000; 2000WO-US14867.	XX
XX	PR 01-JUN-1999; 99US-0322913.	XX
XX	(SCHERING CORP.	XX
XX	xx	XX

OS Mus sp.
 XX WO9619574-A1.
 PN 27-JUN-1996.
 XX 27-NOV-1995; 95WO-US15400.
 PF PR 22-DEC-1994; 94US-0362304.
 XX PA (GEMY) GENETICS INST INC.
 XX PI Tobin JF;
 XX DR N-PSDB; AAT2613.
 XX PT New nucleic acid encoding human interleukin 11 receptor - and
 PT related protein, antibodies, receptor antagonists, etc, useful for
 PT treating and preventing loss of bone mass
 XX PS Example 1; Page 37-40; 54pp; English.
 XX CC The amino acid sequence of the murine Et1-2 gene product is given
 CC in AAR9091. Probes based on the Et1-2 gene (AAT32613) were used
 CC to screen a human cDNA library, yielding a cDNA clone (AAT33278) that
 CC coded for human interleukin-11 receptor (AAR9090), a protein
 CC involved in bone maturation and repair.
 XX SQ Sequence 441 AA;

Query Match	80.5%	Score 1831;	DB 17;	Length 441;
Best Local Similarity	83.1%;	Pred. No. 1..1e-119;		
Matches 340; Conservative	17;	Mismatches 50;	Indels 2;	Gaps 1;

Qy 16 ATAVLASSSPCQAWGPVGVOQGPGRSVKLCCPGVYTAGDPVSWFRDGEPKILQGDPSGL 75
 Db 25 ATAVLSSSSSPCQAWGPVGVOQGPGRPVMLCCPGVSAAGTPVSWFRDGSRLQGDPSGL 84

Qy 76 GHELVLAQADSIDEGVYCCTDGAAGTTTQLGTPPARVEVSOAAADYENFSCTWSPS 135
 Db 85 GIRLVLAQDVSDPDEGYVCQTGDSGMVTLKLGFPARPEVSOAAVDYENFSCTWSPG 144

Qy 136 QISGLPTRYLTSYRKTKLPGAESQRESPSTGPWPCCQDPDPLAASRCVYHGAFFWSEYRINV 195
 Db 145 QVSGLPTRYLTSYRKTKLPGAESQRESPSTGPWPCCQDPDPLAASRCVYHGAFFWSEYRINV 204

Qy 196 TEVNPLGASTRLLDJQSILRPDPGGLRVEVPGVPRIRASWTYPAWSMPCOPHFLIK 255
 Db 205 TEVNPLGASTCCLDVRQLQSLRDPFGGLRVEVPGVPRIRASWTYPAWSMRQPHFLIK 264

Qy 256 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 315
 Db 265 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 324

Qy 316 STGTIPKEIPANGQLHTQ - PEVEPVQDSDAPPRLSQPHPRLDHRDSTEQAVLASIG 373
 Db 325 SNGPLQDEIPDWSQGICQQLEAVVAQEDSPAPARPSLQDPRPLDRDPLQEQAVLASIG 384

Qy 374 ILSFLGLVAGALALGMLWLRRGKGDSKPOFLASVTPVDRPGAPNL 422
 Db 385 IFSCIGLAVAGALALGMLWLRSRGKDGPKQPLAMPIVEKLPGPNL 433

RESULT 9
 ID AAU07726 standard; Protein: 441 AA.
 AC AAU07726;
 XX DT 04-DEC-2001 (first entry)
 XX DE Mouse Et1-2.

XX XX Mouse; interleukin 11 receptor; IL-11R; cytostatic; antianemic;
 KW KW osteopathic; leukopenia; bacterial infection; viral infection;
 KW B cell deficiency; T cell deficiency; hematopoietic cell deficiency;
 KW bone marrow transplantation; immune deficiency; cancer; osteoporosis;
 KW Paget's disease; multiple myeloma; hypogonadism; Et1-2.
 XX OS Mus sp.
 XX PN US6274347-B1.
 XX PD 14-AUG-2001.
 XX PF 10-SEP-1998; 98US-0151102.
 XX PR 14-JUN-1996; 96US-0663584.
 XX PR 15-SEP-1997; 97US-0929846.
 PA (GEMY) GENETICS INST INC.
 XX PA (Tobin J;
 XX DR 2001-549157/61.
 DR N-PSDB; AAS11971.
 XX PT Binding inhibition of interleukin-11 to the human IL-11 receptor,
 PT useful for treatment of anaemia comprises administration of a
 PT composition containing a human IL-11R receptor protein comprising
 PT specific amino acid sequence -
 XX PS Example 1; Column 26-28; 19pp; English.
 XX CC The invention relates to a method of inhibition binding of interleukin-11
 CC (IL-11) to the human IL-11 receptor comprises administration of a
 CC composition containing a human IL-11R receptor protein comprising an
 CC amino acid sequence of 24-365, 102-365, 24-359, 24-345 or 24-324 amino
 CC acids of the human IL-11R protein sequence appearing as AAU07725. The
 CC peptide is used for inhibiting binding of IL-11 to the human IL-11
 CC receptor for the treatment of leukopenia, bacterial and viral
 CC infections, anaemia, B cell or T cell deficiencies such as immune cell or
 CC hematopoietic cell deficiency followed by bone marrow transplantation,
 CC immune deficiency, cancer, regulation of bone maturation and repair, bone
 CC loss (including that associated with osteoporosis post-menopausal
 CC osteoporosis, idiopathic osteoporosis, senile osteoporosis, Paget's
 CC disease, multiple myeloma and hypogonadal conditions). The present
 CC sequence represents mouse Et1-2. The cDNA sequence encoding Et1-2 was
 CC used to design probes which were used to isolate the cDNA encoding Human
 CC IL-11R
 XX SQ Sequence 441 AA;

Query Match	80.5%;	Score 1831;	DB 22;	Length 441;
Best Local Similarity	83.1%;	Pred. No. 1..1e-119;		
Matches 340; Conservative	17;	Mismatches 50;	Indels 2;	Gaps 1;

Qy 16 ATALVASSSSSPCQAWGPVGVOQGPGRSVKLCCPGVYTAGDPVSWFRDGEPKILQGDPSGL 75
 Db 25 ATALVLAQADSDTEGVYCCTDGAAGTTTQLGTPPARVEVSOAAADYENFSCTWSPS 135
 Qy 76 GHBLVLAQADSDTEGVYCCTDGAAGTTTQLGTPPARVEVSOAAADYENFSCTWSPG 144

Qy 136 QISGLPTRYLTSYRKTKLPGAESQRESPSTGPWPCCQDPDPLAASRCVYHGAFFWSEYRINV 195
 Db 145 QVSGLPTRYLTSYRKTKLPGAESQRESPSTGPWPCCQDPDPLAASRCVYHGAFFWSEYRINV 204

Qy 196 TEVNPLGASTRLLDJQSILRPDPGGLRVEVPGVPRIRASWTYPAWSMPCOPHFLIK 255
 Db 205 TEVNPLGASTCCLDVRQLQSLRDPFGGLRVEVPGVPRIRASWTYPAWSMRQPHFLIK 264

Qy 256 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 315
 Db 265 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 324

Qy 316 STGTIPKEIPANGQLHTQ - PEVEPVQDSDAPPRLSQPHPRLDHRDSTEQAVLASIG 373
 Db 325 SNGPLQDEIPDWSQGICQQLEAVVAQEDSPAPARPSLQDPRPLDRDPLQEQAVLASIG 384

Qy 374 ILSFLGLVAGALALGMLWLRRGKGDSKPOFLASVTPVDRPGAPNL 422
 Db 385 IFSCIGLAVAGALALGMLWLRSRGKDGPKQPLAMPIVEKLPGPNL 433

Qy 396 TEVNPLGASTRLLDJQSILRPDPGGLRVEVPGVPRIRASWTYPAWSMPCOPHFLIK 255
 Db 405 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 315

Qy 406 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 324

Qy 407 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 325

Qy 408 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 326

Qy 409 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 327

Qy 410 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 328

Qy 411 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 329

Qy 412 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 330

Qy 413 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 331

Qy 414 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 332

Qy 415 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 333

Qy 416 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 334

Qy 417 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 335

Qy 418 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 336

Qy 419 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 337

Qy 420 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 338

Qy 421 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 339

Qy 422 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 340

Qy 423 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 341

Qy 424 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 342

Qy 425 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 343

Qy 426 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 344

Qy 427 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 345

Qy 428 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 346

Qy 429 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 347

Qy 430 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 348

Qy 431 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 349

Qy 432 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 350

Qy 433 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 351

Qy 434 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 352

Qy 435 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 353

Qy 436 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 354

Qy 437 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 355

Qy 438 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 356

Qy 439 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 357

Qy 440 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 358

Qy 441 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 359

Qy 442 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 360

Qy 443 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 361

Qy 444 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 362

Qy 445 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 363

Qy 446 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 364

Qy 447 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 365

Qy 448 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 366

Qy 449 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 367

Qy 450 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 368

Qy 451 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 369

Qy 452 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 370

Qy 453 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 371

Qy 454 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 372

Qy 455 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 373

Qy 456 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 374

Qy 457 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 375

Qy 458 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 376

Qy 459 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 377

Qy 460 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 378

Qy 461 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 379

Qy 462 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 380

Qy 463 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 381

Qy 464 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 382

Qy 465 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 383

Qy 466 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 384

Qy 467 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 385

Qy 468 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 386

Qy 469 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 387

Qy 470 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 388

Qy 471 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 389

Qy 472 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 390

Qy 473 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 391

Qy 474 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 392

Qy 475 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 393

Qy 476 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 394

Qy 477 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 395

Qy 478 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 396

Qy 479 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 397

Qy 480 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 398

Qy 481 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 399

Qy 482 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 400

Qy 483 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 401

Qy 484 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 402

Qy 485 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 403

Qy 486 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 404

Qy 487 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 405

Qy 488 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 406

Qy 489 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 407

Qy 490 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 408

Qy 491 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 409

Qy 492 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 410

Qy 493 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 411

Qy 494 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 412

Qy 495 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 413

Qy 496 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 414

Qy 497 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 415

Qy 498 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 416

Qy 499 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 417

Qy 500 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 418

Qy 501 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 419

Qy 502 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 420

Qy 503 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 421

Qy 504 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 422

Qy 505 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 423

Qy 506 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 424

Qy 507 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 425

Qy 508 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 426

Qy 509 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 427

Qy 510 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 428

Qy 511 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 429

Qy 512 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 430

Qy 513 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 431

Qy 514 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 432

Qy 515 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 433

Qy 516 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 434

Qy 517 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 435

Qy 518 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 436

Qy 519 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 437

Qy 520 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 438

Qy 521 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 439

Qy 522 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 440

Qy 523 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 441

Qy 524 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 442

Qy 525 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 443

Qy 526 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 444

Qy 527 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 445

Qy 528 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 446

Qy 529 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 447

Qy 530 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 448

Qy 531 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 449

Qy 532 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 450

Qy 533 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 451

Qy 534 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 452

Qy 535 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 453

Qy 536 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 454

Qy 537 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 455

Qy 538 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 456

Qy 539 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 457

Qy 540 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 458

Qy 541 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 459

Qy 542 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 460

Qy 543 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 461

Qy 544 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 462

Qy 545 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 463

Qy 546 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 464

Qy 547 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 465

Qy 548 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 466

Qy 549 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 467

Qy 550 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 468

Qy 551 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 469

Qy 552 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 470

Qy 553 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 471

Qy 554 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 472

Qy 555 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 473

Qy 556 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 474

Qy 557 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 475

Qy 558 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 476

Qy 559 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 477

Qy 560 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 478

Qy 561 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 479

Qy 562 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 480

Qy 563 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 481

Qy 564 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 482

Qy 565 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 483

Qy 566 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 484

Qy 567 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 485

Qy 568 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 486

Qy 569 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 487

Qy 570 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 488

Qy 571 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 489

Qy 572 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 490

Qy 573 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 491

Qy 574 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 492

Qy 575 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 493

Qy 576 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 494

Qy 577 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 495

Qy 578 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 496

Qy 579 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 497

Qy 580 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 498

Qy 581 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 499

Qy 582 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 500

Qy 583 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 501

Qy 584 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 502

Qy 585 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 503

Qy 586 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 504

Qy 587 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 505

Qy 588 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 506

Qy 589 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 507

Qy 590 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 508

Qy 591 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 509

Qy 592 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 510

Qy 593 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 511

Qy 594 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 512

Qy 595 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 513

Qy 596 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 514

Qy 597 FRHQYRAQHPAWSYEWITDAGVPHAVYRVAARDLFELDGTVTWSPEAWGTP 515

Qy 598 FRHQYRAQHPAWSYEWITDAGVPHAV

Db	265	FRLQYRPAQHNPANSTVEP/GLEEVITDAVGLPHAVRSARDLFDGTTWSAWPEAGTP	324
Qy	316	STGTIPKEIPAWGQLHQ - PVEPVQVDSPAPPRPSLQPHPPRLDHDSDSEQVAYLASLG	373
Db	325	STGQLODEIPDWSCGHGQOLEAVQAEDSPAPRPSLQDPDRPLDHRDPL-EQVAYLASLG	384
Qy	374	ILSFLGIGAGALAGLWLRLRGCGKDSSPKPGEFLASVTPVDRPGAPNL	422
Db	385	IFSCIGLAVGALALGWLRLRGCGKDPQKPSLLAPMIPVEKLPGIPNL	433
RESULT 10			
	AAE4614	standard; Protein; 441 AA.	
	ID	AAE4614,	
	AC	AAE4614,	
	XX		
	DT	18-JUN-2002 (first entry)	
	XX		
	DE	Murine Etl-2 protein.	
	XX		
	KW	Murine; Etl-2; interleukin-11 receptor; IL-11R; immune deficiency;	
	KW	haematopoietic progenitor cell; cancer; bone loss; osteoporosis;	
	KW	Paget's disease; multiple myeloma; hypogonadal condition.	
	XX		
	OS	Mus sp.	
	XX		
	PN	US6350855-B1.	
	XX		
	PD	26-FEB-2002.	
	XX		
	PF	15-SEP-1997; 97US-0929846.	
	XX		
	PR	14-JUN-1996; 96US-0663584.	
	PR	22-DEC-1994; 94US-0362304.	
	XX		
	PA	(GEM) GENETICS INST INC.	
	XX		
	PI	Tobin J;	
	XX		
	DR	WPI; 2002-215268/27.	
	DR	N-PSDB; ADD7929.	
	XX		
	CC	Novel isolated human interleukin-11 receptor protein useful in assays	
	CC	to screen for binding agents and for treating immune deficiencies, e.g., osteoporosis -	
	CC		
	PS	Disclosure: Column 25-28; 20pp; English.	
	XX		
	CC	The invention relates to human interleukin-11 receptor (IL-11R). The	
	CC	IL-11R is involved in the regulation of immune system by interaction with IL-11. The IL-11R polypeptide may be used to screen for agents that	
	CC	bind to it or interfere with the binding of IL-11, as diagnostic agent for detecting the expression or presence of IL-11R, IL-11 or cells expressing IL-11R or IL-11. The IL-11R and IL-11R inhibitors may be useful in treatment or modulation of IL-11-related conditions which include immune deficiencies, specifically deficiencies in hematopoietic progenitor cells, or related disorders, cancer and other diseases. It is also believed that IL-11 and IL-11R may play a role in the regulation of bone maturation and repair. As a result, human IL-11R protein and IL-11R inhibitors may be useful in treatment of bone loss including that associated with osteoporosis, post-menopausal osteoporosis, senile osteoporosis, idiopathic osteoporosis, Paget's disease, multiple myeloma and hypogonadal conditions. The present sequence is murine Etl-2, used to illustrate the invention.	
	XX		
	SQ	441 AA;	
	Sequence		
	Query Match	80.5%; Score 1831; DB 23;	Length 441;
	Best Local Similarity	83.1%; Pred. No. 1..119;	Gaps
	Matches 340;	Mismatches 50;	
	Conservative 17;	Indels 2;	
	Qy	16 ATATLASSPCPQAMGGPPGYQGDGRSYKLCCPGVTAGDPWSWFRIDGEPKLGGPSGL 75	

CC (tartrate-resistant acid phosphatase) and bone marrow formation assays
 CC can be used for the identification of IL-11 antagonists. The method not
 CC only inhibits bone resorption and hence bone loss, but also increases the
 CC process of bone formation to increase bone density.

SQ Sequence 379 AA;

Query Match 73.8%; Score 1680; DB 21; Length 379;
 Best Local Similarity 84.2%; Pred. No. 3.1e-109;
 Matches 310; Conservative 17; Mismatches 39; Indels 2; Gaps 1;

Qy 1 MSSSSGSLRSLRVATAVATLVSASSPCPQANWCPGPYQGPGRSVLKCCPGVTAGDPVSNF 60
 Db 1 MSSSSGSLRSLRVATAVATLVSASSPCPQANWCPGPYQGPGRSVLKCCPGVAGTPVSNF 60

Qy 61 RDGEPKLQLQGDGSGLGHVELVLAQAQSTDCEETYICQTLGAGTGTWLLQGYPPARPVSC 120
 Db 61 RDGDSRLQLQGDGSGLGHKLVLQAVDSDPDEGVYCVQFLDGGMWTILKLFPPARPEVC 120

Qy 121 QADYENFSCTWSPSQISLGPLTRYLTSYRKTKVLGADSQRSPSTGPWPQCDPUGAACR 180
 Db 121 QADYENFSCTWSPSQISLGPLTRYLTSYRKTKVLGADSQRSPSTGPWPQCDPUGAACR 180

Qy 181 VVHGAEFWSQYRINTTEVNPLGASTRLLDVSLOSLRDPDQGLRVESYVGPYPRRLRASW 240
 Db 181 VVHGAEFWSQYRINTTEVNPLGASTRLLDVSLOSLRDPDQGLRVESYVGPYPRRLRASW 240

Qy 241 TYPASWPCQPHFLKERLQLRPAQIPAWGQHTQ--PEVEQVDSAPPRSLQPHPRLLD 300
 Db 241 TYPASWRCQPHFLKERLQLRPAQIPAWGQHTQ--PEVEQVDSAPPRSLQPHPRLLD 300

Qy 301 AGTWSWNSPEAWGTPSTGTKEIPAWGQHTQ--PEVEQVDSAPPRSLQPHPRLLD 358
 Db 301 AGTWSWNSPEAWGTPSTGTKEIPAWGQHTQ--PEVEQVDSAPPRSLQPHPRLLD 360

Qy 359 HRDSVEQV 366
 Db 361 HRDPEQL 368

XX PR 18-JUL-2000; 2000IL-0137345.
 XX PR 15-DEC-2000; 2000IL-0140354.
 XX (COMP-) COMPUGEN LTD.
 XX PA WPL: 2002-155037/20.
 XX DR N PSDB; AB139780.
 XX PT One hundred and twenty eight novel nucleic acid sequences, useful for
 PT treating and diagnosing e.g. cancer, asthma and Alzheimer's -
 XX PS Claim 6: Page 254-255; 290pp; English.
 XX ABL39601 to ABL29818 represent novel human-nucleic acid sequences
 CC encoding the proteins given in ABB06167 to ABB06168. The novel sequences
 CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
 CC antiinflammatory, antipsoriatic, ophthalmological, virucide,
 CC vasoconstrictive, antiarteriosclerotic, antidiabetic, dermatological,
 CC anorectic, muscular, anti-HIV, antiinfertility, cardiovascular,
 CC anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiotonic,
 CC immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antilulcer,
 CC antidepressant, gastrointestinal, auroleptic, cerebroprotective,
 CC nootropic and contraceptive activities. The NS can be used in vaccines,
 CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
 CC antibodies from the present invention can be used for treating and
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
 CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
 CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
 CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
 CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
 CC schizophrenia, viral disease, gastric ulcers, stroke,
 CC Alzheimer's disease and as a contraceptive.

SQ Sequence 257 AA;

Query Match 33.9%; Score 771; DB 23; Length 257;
 Best Local Similarity 61.5%; Pred. No. 4.8e-16;
 Matches 160; Conservative 14; Mismatches 42; Indels 44; Gaps 6;

Qy 51 VTAGDPP-VSWPRDGEKFLLQGDPSGJLGHVELVLAQADSTDEGTYICQTLGALG---GT 104
 Db 1 MASGVPELSGVGDGGELVRSPRGVGH---SANGITEDEQQLRAEQPGGRRYSPGV 56

Qy 105 VTLQL-----
 Db 57 CLLPPLPGPLGPGRGPWAARQVREAVLWSQCDRDPARPVSCQADYENFSCTWSPSQI 116

Qy 138 SGLPTRLTYSRKTKVLGADSQRSSSTGPWPQCDPUGAACRYYGAEFWSQYRINVTE 197
 Db 117 SGLPTRLTYSRKTKVLGADSQRSSSTGPWPQCDPUGAACRYYGAEFWSQYRINVTE 176

Qy 198 VNPLGASTRLDVLSLISLRDPQQLRVESYPGYPRRLRASWTFASWPCPTSCSSSV 236
 Db 177 VNPLGASTRLDVLSLISLRDPQQLRVESYPGYPRRLRASWTFASWPCPTSCSSSV 236

Qy 253 LLKFRLQYRPAQHAWSTVE 272
 Db 237 CSTVRRIQPG-PRWSQLD 254

RESULT 13
 AAR06126
 ID ABB06126 standard; Protein; 257 AA.
 XX AC ABB06126;
 XX DT 10-MAY-2002 (first entry)
 XX DE Human NS protein sequence SEQ ID NO:218.
 XX KW Human; cytostatic; osteopathic; gynaecological; neuroprotective;
 KW antineumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
 KW vasoconstrictive; antiarteriosclerotic; antiinflammatory; dermatological;
 KW anorectic; muscular; antiinfertility; cardiovascular; anticoagulant;
 KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiotonic;
 KW antidepressant; antidiabetic; tranquiliser; auroleptic; cerebroprotective;
 KW gastrointestinal; aulicule; antilulcer; cerebroprotective; nootropic;
 KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
 KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
 KW rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma;
 KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
 KW infertility; cardiovascular disease; coagulation disease; hypertension;
 KW ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration;
 KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
 KW gastric ulcer; Alzheimer's disease.

XX OS Homo sapiens.
 XX PN WO200206315-A2.
 XX PD 24-JAN-2002.
 XX DT 17-JUL-2001; 2001WO-IL000553.
 DE DE IL-6R for soluble IL-6R prodn.

AAR22516
 ID AAR22616 standard; Protein; 460 AA.
 XX AC AAR22616;
 XX DT 04-NOV-1992 (first entry)
 XX DE DE IL-6R for soluble IL-6R prodn.

XX	Soluble; sIL-6R.	Db	382 FILRLKQWKSEAEKESKTTSPPPVSLGPLKPTFLVPLTPHSSGSDN 433
XX	Mus musculus.		
XX	Key	RESULT 14	
FH	Peptide	AAB36656	
FT	Region	ID AAB36656 standard; Protein; 460 AA.	
FT		XX	
FT		AC AAB36656;	
FT		XX	
XX		DT 13-MAR-2001 (first entry)	
PN		XX	
XX		DE Mouse IL-6 receptor subunit alpha protein SEQ ID NO:13.	
PD		XX	
XX		KW DNAX cytokine receptor subunit; DCRS2; receptor protein;	
XX		KW modulating cell proliferation; diagnosis; detection; drug screening;	
PR		XX	
XX		KW immunological disorder	
PA		XX	
(CHUS) CHUGAI PHARM CO LTD.		OS Mus sp.	
(TOJ) TOSOH CORP.		XX	
XX		PN WO200073451-A1.	
DR		XX	
DR	WPI; 1992-157367/19.	PD 07-DEC-2000.	
P-PSDB; AAR22616.		XX	
XX		PF 30-MAY-2000; 2000WO-US14867.	
PT		XX	
PT	Recombinant mouse IL-6 receptor - prep. by culturing host	PR 01-JUN-1999;	
PT	transformed by expression vector contg. DNA coding the protein,	XX	
PT	and collecting soluble prod.	PA (SCHERING CORP.	
PS		XX	
PS	Disclosure; Fig 7(1-2); 9pp; Japanese.	PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;	
XX		XX	
CC	The sequence is the full-length mouse IL-6 receptor.	DR WPI; 2001-061536/07.	
CC	The region comprising amino acids 358-385 (see feature table)	XX	
CC	is indicated but not labelled in the sequence given in the	XX	
CC	specification. The sequence is used in the prodn. of a sol.	PT Novel composition comprising DNAX cytokine receptor subunit polypeptide	
CC	mouse IL-6 receptor protein (sIL-6R) which binds specifically to	PT useful for regulating immune system function and for treating	
CC	IL-6 and has no intracellular region.	PT immunological disorders	
XX		XX	
SQ	Sequence 460 AA;	PS Disclosure; Page 13-15; 93pp; English.	
XX		XX	
Query Match	17.4%; Score 395.5; DB 13; Length 460;	Query Match 17.4%; Score 395.5; DB 22; Length 460;	
Best Local Similarity	30.7%; Pred. No. 1.4e-19;	Best Local Similarity 30.7%; Pred. No. 1.4e-19;	
Matches 145; Conservative	58; Mismatches 178; Indels 91; Gaps 25;	Matches 145; Conservative 58; Mismatches 178; Indels 91; Gaps 25;	
QY	1 MSSSCSGLSRVLVAVATLVAASSSSPCPOAWGGPGVQGPGRSVKLCPGVTAGDPVS-- 58	QY 1 MSSSCSGLSRVLVAVATLVAASSSSPCPOAWGGPGVQGPGRSVKLCPGVTAGDPVS-- 58	
Db	2 LTVGCTLLVALLAAPAVAVLGS--CRALEVANTGTVTSLPGATVTLCPGKRAAGNTVTH 59	Db 2 LTVGCTLLVALLAAPAVAVLGS--CRALEVANTGTVTSLPGATVTLCPGKRAAGNTVTH 59	
QY	59 WFRDGPKLQGPD-SGLGHLYLAQADSTDGTCTICOTLDALGGTVTQLGYPPARPV 117	QY 59 WFRDGPKLQGPD-SGLGHLYLAQADSTDGTCTICOTLDALGGTVTQLGYPPARPV 117	
Db	60 WVVSGS---QNRNEWTTGTNTLVLRDQLSDGDYLCL-SLNHBLGVTVPLVDVPBPBPK 114	Db 60 WVVSGS---QNRNEWTTGTNTLVLRDQLSDGDYLCL-SLNHBLGVTVPLVDVPBPBPK 114	
QY	118 VSC-QAADYENFNSCTWSPSQISGLPTRYLTSRKRTVLGADSORRSPTGPMPCP-QDPL 175	QY 118 VSC-QAADYENFNSCTWSPSQISGLPTRYLTSRKRTVLGADSORRSPTGPMPCP-QDPL 175	
Db	115 LSCFRKNPLVNACIWERPSSTS-PTIKAVLPAKKI----NNTNGRSDFQPCQYSQQL 168	Db 115 LSCFRKNPLVNACIWERPSSTS-PTIKAVLPAKKI----NNTNGRSDFQPCQYSQQL 168	
QY	176 GAACRVVIGAEFSQYRI-NTEVNPQGASTRLDV-SLSQSLLRPDEPQGTRVESVPGY 227	QY 176 GAACRVVIGAEFSQYRI-NTEVNPQGASTRLDV-SLSQSLLRPDEPQGTRVESVPGY 227	
Db	169 KSFSCQVEITLEGDKVHVHSICVANSVGSKSSHNEAFHSLK-MVQDPDPANLVSAPIGR 227	Db 169 KSFSCQVEITLEGDKVHVHSICVANSVGSKSSHNEAFHSLK-MVQDPDPANLVSAPIGR 227	
QY	233 PRRRLASRTYPASWPWCOPFLIKFRILQYRPAQHPAWS----TVEPAGLEEVITDAYAG 286	QY 233 PRRRLASRTYPASWPWCOPFLIKFRILQYRPAQHPAWS----TVEPAGLEEVITDAYAG 286	
Db	228 PRWLKVSHQPHETWD-PSYLLQFQLRYR---PVWSKEFTVLLPVAOYOCVHDLRG 282	Db 228 PRWLKVSHQPHETWD-PSYLLQFQLRYR---PVWSKEFTVLLPVAOYOCVHDLRG 282	
QY	287 LPHAVRYSRADFIDLTAGTWSWSPPEAWGTPSTGTPSTGTPKIPA---WGQLIHTQPEVEPVQDSP 343	QY 287 LPHAVRYSRADFIDLTAGTWSWSPPEAWGTPSTGTPSTGTPKIPA---WGQLIHTQPEVEPVQDSP 343	
Db	283 VHVWQVRGKEELDGLQSENSEPEVTGTPWIIE-PRTPAGLWNP-TOVSVE--DS- 335	Db 283 VHVWQVRGKEELDGLQSENSEPEVTGTPWIIE-PRTPAGLWNP-TOVSVE--DS- 335	
QY	344 APPRPSLQPHRLDHED---SVEQAVAVL----SLGISFLGLVAGAIALGLM--- 390	QY 344 APPRPSLQPHRLDHED---SVEQAVAVL----SLGISFLGLVAGAIALGLM--- 390	
Db	336 -----:-----ANHEDQYESSTEATSVLAVQVQESSSMSLTFEL-VAGGSIAFGLLLCV 381	Db 336 -----:-----ANHEDQYESSTEATSVLAVQVQESSSMSLTFEL-VAGGSIAFGLLLCV 381	
QY	391 ---LRLRRGGKD-----GSPKPGFLASV1.PVDRRGAPN 421	QY 391 ---LRLRRGGKD-----GSPKPGFLASV1.PVDRRGAPN 421	

Qy 233 PRLRASWTPASWPQPHELLKFLKERLQYRPAQHPAWS-----TVEPAGLEEVITDAVAG 286
 Db 228 PWLKVTSWQHPPFTWD-PSYUQLFOLYR----PWNSKEETYLILLPVQAQCVIHDALRG 282

Qy 287 LPHAVRSARDFDAGTWSTWSPEANGTPSTGTPKIPA--WCOLHTQDEVEPOVDSP 343
 Db 283 VRHVYQVRGEKEELDGOWSENSEPEVGTGPWAE-PRTPAGILWNP-TQVSVE--DS- 335

Qy 344 APPRPSLQPHPRLLDHDR---SVEQAVLA-----SLGLSFLGLVAGALALGIW--- 390
 Db 336 -----ANHEDQYSSTEATSVLAPQESSSMSLPTFL-VAGGLAFLGLLCV 381

Qy 391 ---LRLRGKKD-----GSPKPGFLASVTPVDRPGAPN 421
 Db 382 FFLRLKQWKWSEAEEKSKTTSPPPPYSLCPPLKPFLLPLTPHSSGSN 433

RESULT 15
 AAR13318 standard; Protein; 460 AA.
 XX
 AC AAR13318;
 XX
 DR 22-OCT-1991 (first entry)
 XX
 DE IL-6 receptor.
 XX
 KW Interleukin.
 XX
 OS Mus musculus.
 XX
 PN JP03155795-A.
 XX
 PD 03-JUL-1991.
 XX
 PF 13-NOV-1989; 89JJP-0292230.
 XX
 PR 13-NOV-1989; 89JJP-0292230.
 XX
 PA (KISHI/) KISHIMOTO C.
 XX
 WP1; 1991-241723/33.
 DR N-PSDB; AAQ13113.
 XX
 PT Receptor protein of mouse IL-6 - prepd. by coding DNA sequence
 PT enabling mass-prod., and useful in study of IL-6 receptor or
 PT immune protein.
 XX
 PS Claim 1; Fig 2; 10pp; Japanese.

CC The amino acid sequence shown encodes mouse IL-6 receptor protein
 CC It can be used for study of the IL-6 receptor or immune mechanism
 CC The protein can be mass-produced by expression of the DNA in host
 CC cells.
 XX
 SQ Sequence 460 AA;

Query Match 16.8%; Score 382.5%; DB 12; Length 460;
 Best Local Similarity 30.3%; Pred. No. 1.e-18;
 Matches 143; Conservative 58; Mismatches 180; Indels 91; Gaps 25;

Qy 1 MSSSCSGLSRIVAVATALVASSSPCQAWGGPPGYQXQGRSVKLCCPGTAGDPVSS-
 Db 2 LTVGCCTLVALLAAPAVALVGS-CRALEYANGTTSLPAVTVLICPGREAAGNTIH 59

Qy 59 WFRDGEPKLQGPD-SGLGHIELVLAQADSTDEGYTCQTLGALGGTYTQLGYPPARPV 117
 Db 60 WYVSGS---QNREWTTGNTRVLDRYQLRTEGDYLCS-LNDHLVGTVPVLDVPPPEPK 114

Qy 118 VSC-QAADYENFSCTWSPSQSLGLPRLYRLTSYRKRTVGLGASQRRLPSTGWPWPCP-QDPL 175
 Db 115 LSCFRKNPLVNAICERWPSSTS-PTTKAVLFAKKI----NTTNGKSDFQVPCQYSQQL 168

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